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Result
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                                                                           August 29, 2001, 15:04:42; Search time 1774.1 Seconds (without alignments) 130.780 Million cell updates/sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                    tal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                            1344157 seqs, 7733874588 residues
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Maximum Match 100%
Listing first 45 summaries
                                                    OM nucleic - nucleic search, using sw model
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15
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Database :

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A70378 Sequence 8 AX095547 Sequence M94144 Mus musculu M64874 Mouse inter D88111 Homo sapien AF115754 Gequus cab G65440 std3388M5_1 AF043127 Homo sapi

A/U3/ AX095547 MUSAIC2A09 MUSIL4R07 D88111 ECIL/R1 G65440 3 HSIL/R5

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Query Match Length DB

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

30-MAR-2001

PAT

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (Joases 1 to 21)
Lander, E.S., Gargill, M., Ireland, J.S., Bolk, S., Daley, G.Q. and McCarthy, J.J.
Single nucleotide polymorphisms in genes
Patent: WO 0118250-A 755 15-MAR-2001;
WHITEBEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US); Millennium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     92.0%; Score 13.8; DB 10;
86.7%; Pred. No. 7.2e+02;
ive 2; Mismatches 0;
                                                                                                 AX095547 21 bp DNA
Sequence 725 from Patent WO0118250.
AX095547
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/db_xref="taxon:9606"
1 c 11 g
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Location/Qualifiers
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Nicola,N.A., Fabri,L., Farley,A., Nash,A., Willson,T., Rakar,S.,
Slang,J., Alexander,W., Hilton,D.J., Kojima,T., Maeda,M. and
Kikuchi,Y.
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/organism="unidentified"
/db_xref="taxon:32644"
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121102
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AC072998
AC030504
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Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 160)
Gorman, D.M., Itoh, N., Jenkins, N.A., Gilbert, D.A., Copeland, N.G. and Miyajima, A.
                                                                                                                                                                                                                                                                                                                                                  Chromosomal localization and organization of the murine genes encoding the beta subunits (AIC2A and AIC2B) of the interleukin 3, granulocyte/macrophage colony-stimulating factor, and interleukin
     27-APR-1993
MUSAIC2A09 160 bp DNA ROD 27-APR-19' MUSA musculus IL-3 receptor B-subunit (AIC2A) gene, exon 10. M94144 GI:191815
                                                                                                                                                             Mus musculus (strain BALB/c, sub_species domesticus) DNA.
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J. Biol. Chem. 267, 15842-15848 (1992)
92348451
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/db_xref="taxon:9606"
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Nishikawa, N.
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                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I (Dases 1 to 207)
Wrighton, N., Campbell, L.A., Harada, N., Miyajima, A. and Lee, F. The murine interleukin-4 receptor gene: genomic structure, expression and potential for alternative splicing Growth Factors 6 (2), 103-118 (1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (strain:HeLa) DNA, clone_lib:libraly of clones containing poly(dG)poly(dC)library clone:pHGC40L.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /standard_name="'IL-4R'"
/note="'approx. 1.4kb 3' of segment 6'; 'interleukin-4
receptor'; putative"
                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                 06-MAY-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="comparing genomic to cDNA; found in Balb/c'
                                                                                                                                                                                                                               Mus musculus (strain BALB/c, sub_species domesticus) DNA.
                           0;
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                            Indels
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                                                                                                                                        MUSILAR07 207 bp DNA ROD MOUSE interleukin 4 receptor gene, exon 7. M64874 M64874 GI:198354
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Pred. No. 7.9e+02;
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Pred. No. 8e+02;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                             /strain="BALB/c"
/sub_species="domesticus"
/db_xref="taxon:10090"
/cell_type="sperm"
<1. .25
/note="putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              55

    207
    organism="Mus musculus"

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/note="putative"
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183. .>207
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80.0%;
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           80.08;
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Best Local Similarity 80.0
Matches 12; Conservative
            Best Local Similarity 80.0
Matches 12; Conservative
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132 GCTCCACTCGCTCCA 118
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160 ACTCCACTCACTCCA 146
                                                    1 RCTCCAYTCRCTCCA 15
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Caetano, A.R., Lyons, L.A., Laughlin, T.F., O'Brien, S.J., Murray, J.D.
and Bowling, A.T.
                                                                                                                                                                                                                                                                                      3 (sites)
Nishikawa,N., Kanda,N., Oishi,M. and Kiyama,R.
Nishikawa,N., Kanda,N., Oishi,M. and Kiyama,R.
Genrichment of oligo(dG).Oligo(dC)-containing fragments from human genomic DNA by Mg 2+-dependent triplex affinity capture
Nucleic Acids Res. 25 (9), 1701-1708 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Murray, J.D.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Perissodactyla; Equidae; Equus.

1 (bases 1 to 248)

Caetano,A.R., Lyons,L.A., Laughlin,T.F., O'Brien,S.J., Murray,J.D

and Bowling,A.T.

Equine synteny mapping of comparative anchor tagged sequences

(CATS) from human Chromosome 5

Mamm. Genome 10 (11), 1082-1084 (1999)
                                      Naoko
Direct Submission
Submitted (28-SEP-1996) to the DDBJ/EMBL/GenBank databases. Naok
Nishikawa, Univ. Tokyo, Ins. Mol. Cell. Biosci.; Yayoi 1-1-1,
Bunkyo-ku, Tokyo 113, Japan (Tel:03-3812-2111(ex.7877),
Pax:03-3818-9437)
2 (bases 1 to 213)
2 (bases 1 to 213)
Mishikawa, N., Oishi, M. and Kiyama, R.
Enrichment of poly(dG): poly(dC)-containing fragments from human genomic DNA by Mg2+-dependent triplex affinity capture
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Submitted (22-DEC-1998) Veterinary Genetics Lab., University of
California Davis, One Shields Ave., Davis, CA 95616, USA
Location/Qualifiers
1. .248
/organism="Equus caballus"
/db_xref="taxon:9796"
81 a 43 c 58 9 66 t
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Equus caballus interleukin-7 receptor (IL/R) gene, partial
sequence.
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/clone_lib="libraly of clones containig
poly(dG)poly(dC)library"
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80.0%; Pred. No. 8e+02;
ive 3; Mismatches
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/strain="HeLa"
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Puel, A., Ziegler, S.F., Buckley, R.H. and Leonard, W.J.
Direct Submission
Submitted (15-JAN-1998) Immunology, Virginia Mason Research Center, 1000 Seneca St., Seattle, WA 98101, USA
Location/Qualifiers
                                                                                                                                                                                                                                            Homo sapiens
Bukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 403)
Puel, A., Zitegler, S.F., Buckley, R.H. and Leonard, W.J.
Defective IL/R expression in T(·)B(+)NK(+) severe combined immunodeficiency
                                                                                                                                      HSIL7R5 403 bp DNA PRI 05-DEC-1998
Homo sapiens interleukin-7 receptor precursor (IL7R) gene, exon
AF043127
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Leonard, W.J., Noguchi, M. and McBride, O. Wesley.
Methods for diagnosis of XSCID and kits thereof
Patent: US 5518880-A 73 21-MAY-1996;
Location/Qualifiers
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Pred. No. 8.3e+02;
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Pred. No. 8.2e+02;
3; Mismatches 0;
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   Mismatches
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/organism="Homo sapiens"
/db_xref="taxon:9606"
140. .308
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ı 127 c 110 g
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80.0%;
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/number=5
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Best Local Similarity 80.0
Matches 12; Conservative
 12; Conservative
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265 ACTCCATTCACTCCA 251
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Unclassified.
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VERSION
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Primer A: GAAGTGCAGAGGGAAACTGC
Primer B: GACTCAGACCAGGTCCTGGA
STS size: 367
PCR Profile:
                                                                                                                                                                                                                                                                                                                           Dawson, E., Chen, Y., Hunt, S. and Dunham, I.
Extraction and analysis of SNP data from genomic sequence of human chromosome 22
                                                                                                                                                                                                                                                                                       Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 367)
                                                                                                                                                                  G65440 367 bp DNA STS 19-JUL-2000 stdJ388M5_151462 chromosome 22 genomic clone Homo sapiens STS genomic clone 388M5, sequence tagged site.
                                 Gaps
                               ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Presoak: 94 degrees C for 5.00 minutes Denaturation: 93 degrees C for 30 seconds Extension: 72 degrees C for 30 seconds PCR Cycles: 35 PCR Cycles: 35 PCR Cycles: 75 degrees C for 5 minutes Thermal Cycler: MJ Research (DNA Engine Tetrad)
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Score 13.8; DB 7; Length 248;
Pred. No. 8e+02;
3; Mismatches 0; Indels
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/db_xref="taxon:9606"

/clone="388M5"

/clone="388M5"

/clone=lib="chromosome 22 genomic clone"

1. .367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 13.8; DB 54;
Pred. No. 8.2e+02;
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Location/Qualifiers
1. .367
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2-mercaptoethanol: 10mM
Taq Polymerase: 0.04 units/ul
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each 0.5 mM
each 500 uM
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96 g
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67 mM fris-HCl
16.7 mM (NH4)2SO4
pH: 8.8
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121 c 96
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80.0%;
 92.0%;
80.0%;
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                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1999)
Synonyms: stSG73865
Contact: Ian Dunham
Query Match 92.0
Best Local Similarity 80.0
Matches 12; Conservative
                                                           1 RCTCCAYTCRCTCCA 15
                                                                             Total Vol:
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Pest Local Similarity
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                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                     1 (bases 1 to 490)
Noguchi,M., Adelstein,S., Cao,X. and Leonard,W.J.
Characterization of the human interleukin-2 receptor gamma chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (01-SEP-1999) Phytopathologie, INRA, route de St Cyr, 78026 Versailles, France
                                                                                                                           HUMIL2RG05 490 bp DNA PRI 06-JAN-1995
Human interleukin 2 receptor gamma chain (IL2RG) gene, exon 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
 Gaps
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T4 cDNA library under conditions of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Fungl; Ascomycota; Pezizomycotina; Leotiomycetes; Helotiales; Sclerotiniaceae; Botryotinia. 1 (bases I to 537)
Bitton,F., Levis,C., Fortini,D., Pradier,J.M. and Brygoo,Y. Direct Submission
                                                                                                                                                                                                              Homo sapiens (tissue library: Charon 4A) fetus liver DNA.
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93293887
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Pred. No. 8.3e+02;
3; Mismatches 0;
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 Mismatches
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interleukin 2 receptor gamma chain.
5 of 8
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Botryotinia fuckeliana.
Botryotinia fuckeliana
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                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="liver"
/tissue_lib="Charon 4A"
                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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nitrogen deprivation.
AL117163
AL117163.1 GI:5832379
3;
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126. .288
/gene="IL2RG"
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80.0%;
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127 c
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Conservative
                                                      254 GCTCCATTCACTCCA 240
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254 GCTCCATTCACTCCA 240
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                          1 RCTCCAYTCRCTCCA 15
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Nixon,J., Morrison,H.G., McArthur,A.G., Eakin,N.O., Kim,U., Crocker,M.C., Hinkle,G., Holder,M.E. and Sogin,M.L. Direct Submission

Direct Submission

Submitted (07-JUN-2000) Josephine Bay Paul Center for Comparative Molecular Biology and Evolution, Marine Biological Laboratory, 7 mBi. Street, Woods Hole, MA 02543-1015, USA

* NOTE: This record contains I individual

* sequencing reads that have not been assembled into

* contigs. Runs of N are used to separate the reads

* and the order in which they appear is completely

* arbitrary. Low-pass sequence sampling is useful for

* identifying clones that may be gene-rich and allows

* overlap relationships among clones to be deduced.

* However, it should not be assumed that this clone

* Will be sequenced to completion. In the event that

* the record is updated, the accession number will
CP 5706 91057 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web: www.genoscope.cns.fr)
The cDNA library to be analyzed within the framework of this project was created using a Botrytis cinerea strain which was grown under conditions of nitrogen deprivation, which is the normal situation for B. cinerea during its development on its host plant. The library was produced in an oriented direction, in the pBSII vector.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AC072998 572 bp DNA HTG 07-JUN-2000 Giardia intestinalis clone NJ4660 strain WB-C6, LOW-PASS SEQUENCE
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Morrison, H.G., McArthur, A.G., Nixon, J., Eakin, N.Q., Kim, U., Crocker, M.C., Hinkle, G., Holder, M.E. and Sogin, M.L. Giardia: a model for ancient eukaryotic genome analysis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 537;
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                                                                                                                                                                                                                                                                       1. .537
/organism="Botryotinia fuckeliana"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 13.8; DB 14;
Pred. No. 8.3e+02;
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                                                                                                                                                                                                                                                                                                                                                                                        /note="Genoscope sequence
46 c 178 g 176
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/clone="NJ4660"
                                                                                                                                                                                                                                            Location/Qualifiers
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80.0%;
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Giardia intestinalis
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Best Local Similarity 80.0
Matches 12; Conservative
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/translation="KPGEDGGLPTKYTLTYHKEGETTTHECPDYITSGPNSCYFNKKH
TSIWTHYITTINATNENGSSSSDPRYVTLTYTVEPDPPVNLSLELKOPEDKKTYLWIK
WYPPTLVDVRSGWLTLOYEIRLKPERATEWETHFAGLOTOFKILSLYPGGKYLVQVRC
KPDHGWWSEWSPKRTQIPUDISMKOTIVWIFVAVLSAVICLIMVAAVALKGHSMYT"
159 c 145 g 153 t
                   Douglas,D.A., Houde,A., Song,J.H., Farookhi,R., Concannon,P.W. and
Murphy,B.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Ursidae; Ursus.

1. (bases 1 to 681)
Howell-Skalla,L.A., Bunick,D., Bleck,G.T., Nelson,R.A. and Bahr,J.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (19-JUL-1999) Curriculum in Toxicology, University of North Carolina, MD-72, US EPA, Research Triangle Park, NC 27711,
                                                           Luteriopic hormone receptors in the ovary of the mink (Mustela vison) during delayed implantation and early-postimplantation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cloning, sequence analysis, and seasonal mRNA expression of the extracellular region of the lutefinizing hormone receptor (LHr), follicle-stimulating hormone receptor (FSHr), and prolactin receptor (PRLr) genes in the testis of the black bear (Ursus
                                                                                                                                                                                                                               Direct Submission
Submitted (08-OCT-1997) Agriculture and Agri-Food Canada, Food
Research and Development Centre, 3600 Casavant Blvd. West,
St-Hyacinthe, Quebec J2S BE3, Canada
Location/Qualifiers
1. .652
//Organism="Mustela vison"
//db.xref="taxon:9667"
//lissue_type="testis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AF169792 681 bp mRNA MAM 07-SEP-2000
Ursus maritimus prolactin receptor mRNA, partial cds.
AF169792
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Douglas, D.A., Song, J. H., Houde, A. and Murphy, B.D.
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Pred. No. 8.4e+02;
3; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="prolactin receptor"
                                                                                                                       Biol. Reprod. 59 (3), 571-578 (1998)
98384190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /protein_id="AABB8899.1"
/db_xref="GI:2688975"
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Howell-Skalla, L.A. and Bahr, J.M.
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1. .681
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<1. .>652
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80.0%;
    1 (bases 1 to 652)
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Best Local Similarity 80.0
Matches 12; Conservative
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Eukaryota; Diplomonadida; Hexamitidae; Giardiinae; Giardia.

(bases 1 to 585)

Morrison, H.G., McArthur, A.G., Nixon, J., Eakin, N.Q., Kim, U.,
Crocker, M.C., Hinkle, G., Holder, M.E. and Sogin, M.L.
Giardia: a model for ancient eukaryotic genome analysis

L Unpublished

(Dases 1 to 585)

Eakin, N.Q., Morrison, H.G., McArthur, A.G., Nixon, J., Kim, U.,
Crocker, M.C., Hinkle, G., Holder, M.E. and Sogin, M.L.
Direct Submission

L Submitted (02-ARR-2000) Josephine Bay Paul Center for Comparative Molecular Biology and Evolution, Marine Biological Laboratory, 7

MBL Street, Woods Hole, MA 02543-1015, USA

* NOTE: This record contains 1 individual

* sequencing reads that have not been assembled into

* contigs. Runs of N are used to separate the reads

* and the order in which they appear is completely

* arbitrary. Low-pass sequence sampling is useful for

* identifying clones that may be gene-rich and allows

* overlap relationships among clones to be deduced.

* However, it should not be assumed that this clone

* will be sequenced to completion. In the event that

* the record is updated, the accession number will
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Mammalia, Eutheria, Carnivora, Fissipedia, Mustelidae, Mustela.
                        Gaps
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Mustela vison prolactin receptor (PRLr) mRNA, partial cds.
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  Pred. No. 8.3e+02;
3; Mismatches 0;
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Pred. No. 8.3e+02;
3; Mismatches 0;
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/clone="E10461"
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HTG; HTGS_PHASE0.
Glardia intestinalis.
Glardia intestinalis.
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80.0%;
80.08;
Best Local Similarity 80.(
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3JT, UK.

Tel: +44 131 650 6760

Fax: +44 131 670 5450

Emali: mark.blaxterded.ac.uk

The Ascaris suum EST dataset (including the ASC clustering information) is available on the www at http://www.ed.ac.uk/(tilde.) mbx/AscarisWeb/AscarisEST.html PCR PRimers

FORMARD: M13 Reverse (AGCGGATAACAATTTCACACAGGA)

BACKWARD: M13 Reverse (AGCGGATAACAATTTCACACAGGA).

Seq primer: M13 Reverse (AGCGGATAACAATTTCACACAGGA).

LOCATION/Qualifiers

115
                                                                                                                                                                                                      Bukaryota; Matazoa; Nematoda; Chromadorea; Ascaridida; Ascaridoidea; Ascarididae; Ascaris:
1 (bases 1 to 315)
1 (bases 1 to 315)
1 Daub, J., Geary, T. and Blaxter, M.
A survey of genes expressed in the parasitic nematode Ascaris suum Contact: Blaxter M.
Institute of Cell, Animal and Population Biology
University of Edinburgh
Ashworth Labs, King's Buildings, West Mains Road, Edinburgh, EH9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AW165758 315 bp mRNA EST 12-NOV-1999 MBASBWA080M13R Ascaris suum (parasitic nematode) body wall muscle and hypodermis Ascaris suum cDNA clone MBASBWA080 5', mRNA
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/organism="Ascaris suum" ./
/db_xerf="taxon:6253"
/clone=!MABABWA080!
/clone=lib="Ascaris suum (parasitic nematode) body wall
muscle and hypodermis"
                                                                                  sequence.
AW165758
AW165758.1 GI:6382633
EST.
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                                                                                                                                                                        pig roundworm.
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.; 0 92.0%; Score 13.8; DB 112; Length 315; 80.0%; Pred. No. 2.8e+03; Live 3; Mismatches 0; Indels 0; Query Match 92.0 Best Local Similarity 80.0 Matches 12; Conservative 1 RCTCCAYTCRCTCCA 15

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191 ACTCCACTCACTCCA 205
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.

1. (bases 1 to 302)

8. Konno, H., Alzawa, K., Akahira, S., Akiyama, J., Carninci, P., Endo, T.,
Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Hori, F.,
1811, Y., Ishikawa, T., Itoh, M., Izawa, M., Radota K., Kagawa, T., Kai,
C., Kawai, J., Kikuchi, N., Kojim, Y., Koya, S., Kusakabe, M., Natuchi, N., Salto, H., Sano, M., Sato, K., Shibata, Y., Shigemoto, Y., Shiraki, T., Saoabe, Y., Sugahara, Y., Suzuki, H.,
Suzuki, H., Takahashi, F., Tateno, M., Tominaga, N., Tsunoda, Y.,
Watahiki, A., Watanabe, S., Yamamura, T., Yasunishi, A., Yokota, T.,
Yoshiki, A., Watanabe, S., Yamamura, T., Yasunishi, A., Yokota, T.,
RIKEN Mouse ESTS (Konno, H., et al. 1999)

N. Unpublished (1999)
Contact: Yoshihide Hayashizaki
Genome Exploration Research Group, Life Science Tsukuba Center,
Genome Science Laboratory
The Institute of Physical and Chemical Research (RIKEN), Genomic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: genome-res@rtc.riken.go.jp,
WLihttp://genome.rtc.riken.go.jp,
Saski,N., Izawa,M., Watahiki,M., Ozawa,K., Tanaka,T., Yoneda,Y.,
Matsuura,S., Carninci,P., Muramatsu,M., Okazaki,Y. and Hayashizaki
                                                                                                                                                                                                                                                                                                                                                         AV298115 302 bp mRNA bost AV298115 RIKEN full-length enriched, 8 days embryo Mus musculus cDNA clone 5730454J22 3', mRNA sequence.
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/clone_llb="RIKEN full-length enriched, 8 days embryo"
/sex="mixed" days embryo"
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5' end: SalI; 3' end: BamHI."
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Tel: +81-298-36-9013
Fax: +81-298-36-9098
                                                                                                                                                           3; Mismatches
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  Cloning sites,
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AV298115
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                                                                                                            92.0%;
80.0%;
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Best Local Similarity
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AV298115
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l (bases 1 to 313)
Zabarovska, P.R., Glatullin, R., Podowski, R.M., Zabarovska, V.V., Xie
L., Muravenko, O. V., Kozyrev, S., Petrenko, L., Skobeleva, N., Li, J.,
Protopopov, A., Kashuba, V., Ernberg, I., Winberg, G. and Wahlestedt, C.
NotI clones in the analysis of the human genome
Nucleic Acids Res: 28 (7), 1635-1639 (2000)
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/note="Site_1: Sall; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5]
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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NDG-223C Human NotI clones Homo sapiens genomic, DNA sequence.
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Pred. No. 2.8e+03;
3; Mismatches 0;
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/db_xref="taxon:9606"
/clone_lib="Human NotI clones"
148 c 74 q 43 t.
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Rarolinska Institute
17177 Stockholm, Sweden
Tel: +46-8-728-6372
Fax: +46-8-337983
Email: Raf. Podowski@cgr.ki.se
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Location/Qualifiers
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/sex="male"
                                    Mus musculus
Eukaryota; Metazoa;
                                                                           Mammalia; Eutheria;
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                                                                                                    Email: genome-resertc.riken.go.jp,
URL: http://genome.rtc.riken.go.jp,
URL: http://genome.rtc.riken.go.jp,
Carninci,P. Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki,N., Okazaki,Y., Muramatsu,M. and Haysahizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki,
Y. and Hayashizaki,Y.
Automated filtration-based high-throughput plasmid preparation
system. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
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BB024897.1 GI:8198974
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                 The Institute of Physical and Chemical Research (RIKEN), Genomic
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/dev_stage="13 days embryo"
/lab_host="DH10B"
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/clone="5930436B16"
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 Genome Science Laboratory
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80.0%;
                                                                     Tel: +81-298-36-9013
Fax: +81-298-36-9098
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Matches 12; Conservative
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                                    Sciences Center
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E (Annuality Burnella) Scillogidality Mullides; Konno, H., Alzawa, K., Akahira, S., Akiyama, J., Arakawa, T., Carninci, Hirozane, T., Hori, F., Ishi, Y., Ishikawa, J., Ishikawa, T., Itoh, M., Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N., Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kusakabe, M., Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y., Shigemoto, Y., Shinagawa, A., Shirana, M., Salo, K., Shibata, Y., Shigemoto, Y., Shinagawa, A., Takahashi, F., Tominaga, N., Suzuki, H., Tagawa, A., Takahashi, T., Yamanusa, T., Yano, Y., Yano, K., Yasusishi, A., Yokota, T., Yoshida, K., Yoshiki, A., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.
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URL:http://genome.rtc.riken.go.jp,
Carninci.P., Nishiyama,Y., Westover.A., Itoh,M., Nagaoka,S., Sasaki,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
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Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J., Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.
                                    Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Chordata; Craniata; Vertebrata; Euteleostomi;
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Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
Please visit our web site (http://genome.rtc.riken.go.jp) for further details.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: +81-298-36-9013
Fax: +81-298-36-9098
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/dev_stage="adult"
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/clone="5330424007"
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Kim,C.Y., Cheon,S.Y. and Cho,M.J.

Isolation and Characterization of Fungal Elicitor Responsive Rice
Genes by mRNA Differential Display
Unpublished (1998)

Contact: Kim, Cha Young
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        AF061117 Rice Millyang 117 suspension culture mRNA Oryza sativa AF061117
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/clone="r25109"
/clone_lib="Rice Millyang 117 suspension culture mRNA"
/note="suspension culture"
66 c 70 g 84 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           900 Gajwa-dong, Chinju, Kyeong-nam 660-701, Korea
Email: choslab@nongae.gsnu.ac.kr.
Location/Qualifiers
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Pred. No. 2.8e+03;
3; Mismatches 0;
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URL:http://genome.rtc.riken.go.jp,
Carninoi.p., Nishlyama.Y., Westover, A., Itoh, M., Nagaoka, S., Sasaki
Carninoi.p., Nishlyama.Y., Mestover, A., Itoh, M., Nagaoka, S., Sasaki
N., Okazaki, Y., Muramatu, M. and Hayashizaki, Y.
Thermostabilization and thermoactivation of thermolabile enzymes by
trehalose and its application for the synthesis of full length
cDNA. Proc. Nall. Acad. Sci. U.S. A. 95 (2), 520-524 (1998)
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Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki,
Y. and Hayashizaki, Y.
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                                                                                                                                                 Contact: Yoshihide Hayashizaki
Genome Exploration Research Group, Life Science Tsukuba Center,
Genome Science Laboratory
The Institute of Physical and Chemical Research (RIKEN), Genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
Garnincl, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Please visit our web site (http://genome.rtc.riken.go.jp) for further details.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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/organism="Mus musculus"
/organism="Mus musculus"
/drain="537BL/63"
/db_xref="taxon:10090"
/dclone="53942bL02"
/clone="153942bL02"
/clone_1ib="RIKEN full-length enriched, adult male
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
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Pred. No. 2.8e+03;
3; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                             3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: +81-298-36-9013
Fax: +81-298-36-9098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FLC I. Cloning sites, 5' ^{\prime} 17 c ^{\prime} 57 g ^{\prime}
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80.0%;
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Best Local Similarity 80.0
Matches 12; Conservative
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184 ACTCCATTCACTCCA 170
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                                                                                                                                                                                                                                                                        Sciences Center
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//tissue_type="Tcell"
/dev_stage="Mad CD4+ cells"
/lab_host="SOLR (kanamycin resistant)"
/lab_host="SOLR (kanamycin resistant)"
/lab_host="SolR (kanamycin resistant)"
/lab_host="Site_2: XhoI; Cloned undirectionally. Primer:
CORI; Site_2: XhoI; Cloned undirectionally. Primer:
Oligo dr. M90 CD4+ cells. Average insert size: 1.0 Kb;
Uni-ZAP XR Vector; -5' adaptor sequence: 5' GAATTCGGCACGAG
3' -7' 0 C
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                                                                                                               The factor of th
                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Marra MyMouse EST Project
WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty free through LLNL; contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                     The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:10090"
/clone="IMAGE:972918"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Putative full length read vector to vector length is 288 Seq primer: -28ml3 revl ET from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                         Waterston, R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Exa: 402 762 4360
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and trimmed with phred
and —minmatch 12 options.
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Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A., Smith, T.P.L., Casas, E. Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Laegreid, W.W. and Keele, J.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Design and use of two pooled tissue normalized cDNA libraries for EST discovery in swine Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             v121g04.rl Stratagene mouse Tcell 937311 Mus musculus CDNA clone IMAGE:972918 5' similar to gb:M29697 Mouse interleukin-7 receptor AA562009
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/db.xref="taxon:9823"
/clone_lib="Mexor of 10"
/tlsue_type="pooled"
/lab_host="DH10B"
/note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
Library made from pooled tissue from day 11, 13, 15, 20, and 30 embryos."
                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                     AW417497 275 bp mRNA EST
4258 MARC 1PIG Sus scrofa cDNA 5', mRNA sequence.
AW417497.1 GI:6945379
                                               Indels
       Pred. No. 2.7e+03;
3; Mismatches 0;
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Plate: 20 row: K column: 3
Seq primer: ATTTAGGTGACACTATAG.
Location/Qualifiers
1..275
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⁄organism≂"Sus scrofa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FORWARD: AGGAAACAGCTATGACCAT
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       80.08;
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Best Local Similarity 80.0
Matches 12; Conservative
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Konno, H., Aizawa, K., Akahira, S., Akiyama, J., Arakawa, T., Carninci, P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Hori, F., Ishii, Y., Ishikawa, J., Ishikawa, T., Itoh, M., Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N., Isawa, H., Koʻjima, Y., Kondo, S., Koya, S., Kurihara, C., Kusakabe, M. Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y., Ono, T., Owa, C., Saito, H., Sakai, C., Sato, K., Shibata, K., Shigemoto, Y., Shinagawa, A., Takahashi, F., Tominaga, N., Suzuki, H., Yanoda, Y., Watanaki, A., Takahashi, F., Tominaga, N., Toya, T., Yanoda, Y., Watanaki, S., Yamamura, T., Yamanatsu, M., Muramatsu, M., and Hayashizaki, Y. Yoshida, K., Yoshiki, A., Yoshino, M., Muramatsu, M., Matanaki, Y., Et al., Doppole STS (Konno, H., et al.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: genome-resertc.riken.go.jp,
URL:http://genome-rtc.riken.go.jp,
URL:http://genome-rtc.riken.go.jp/
Carhinci.P. Nabinyama.Y. Westover,A., Itoh,M., Nagaoka,S., Sasaki
,N. Okazaki,Y. Muramatsu,M and Hayashizaki,Y
Thermostabilization and thermoactivation of thermolabile enzymes by
trehalose and its application for the synthesis of full length
cDNA, Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki
,Y. and Hayashizaki,Y.
Automated filtration-based high-throughput plasmid preparation
system. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
19-44 (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Site_1: Sall; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5]
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/dev_stage="12 days embryo"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                             Contact: Yoshihide Hayashizaki
Contact: Yoshihide Hayashizaki
Genome Exploration Research Group, Life Science Tsukuba Center,
Genome Science Laboratory
The Institute of Physical and Chemical Research (RIKEN), Genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="RIKEN full-length enriched, 12 days embryo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: +81-298-36-9013
Fax: +81-298-36-9098
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/clone="6720436D12"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 256)
Zhao,S., Adams,M.D., Nierman,W., Malek,J., Shizuya,H., Simon,M. and Venter,J.C.
Use of BAC End Sequences from CalTech Libraries for Sequence-Ready Unpublished (1997)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: hbe@tigr.org Clones are available from Research Genetics (info@resgen.com). BAC
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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BBD51888 RIKEN full-length enriched, 12 days embryo male wolffian
duct Mus musculus cDNA clone 6720436D12 3' similar to U01135 Mus
musculus B6D2F1 clone 2A-1 mRNA, mRNA sequence.
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http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seg primer: M13-21
Class: BAC ends.
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                                                                                                                                                                                                                                             AQS48570 256 bp DNA GSS 28-MAY-1999
CITBI-E1-2635F16.TF CITBI-E1 Homo sapiens genomic clone 2635F16,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Shaying Zhao, William Nierman, Mark Adams Department of Eukaryotic Genomics
The Institute for Genomic Research
712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0208
Fax: 301 838 0208
                  Indels
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                  Mismatches
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/clone="2635F16"
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/note="Vector: pBel
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/dev_stage="Adult"
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Fax: 314 286 1810
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43 GCTCCACTCACTCCA 29
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I (bases 1 to 201)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?ti=&t2-MR2-BT0590-100
300-118-c08_lst3=20000-031-08t4=1)
Seq primer: puc 18 forward
High quality sequence stops: 201.
Location/Qualifiers
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v0.980904.e. Vector identified by cross_match with the -minscore 18
                                                                                                                                                                                                                                                                /note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI; Library made from pooled tissue from marrow, alveolar macrophage, ovary, fetal semitendonosus muscle, and fetal longissimus muscle."
1 59 59 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BE076128 201 bp mRNA EST 09-JUN-2000 MR2-BT0590-100300-118-c08_1 BT0590 Homo sapiens cDNA, mRNA
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Pred. No. 2.6e+03;
3; Mismatches 0; I
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/db_xref="taxon:9606"
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                                                                                                                                                    1. .173 //Organism="Bos taurus"
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/clone_lib="MARC 3BOV"
                                                     FORWARD: AGGAAACAGCTATGACCAT
BACKNARD: GTTTTCCAGTACAGGACG
Plate: 40 row: J column: 24
Seq primer: ATTTAGGGTGACACTATAG.
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/lab_host="DH10B"
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MEDLINE
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/note-"Organ: breast; Vector: puc18; Site_1: Smal; Site_2: Smal; A min-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196, 716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
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1 (bases 1 to 248)

Marra, M., Hiller, L., Kucaba, T., Martin, J., Beck, C., Wylie, T.,
Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y.,
E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R.,
The WashU-NCI Mouse EST Project 1999
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AISO5954 248 bp mRNA EST 11-MAR-1999 vl21f12.x1 Stratagene mouse Tcell 937311 Mus musculus CDNA clone IMAGE:972911 3' similar to gb:M29697 Mouse interleukin-7 receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
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/db_xref="taxon:10090"
/clone="IMAGE:972911"
/clone_lib="Stratagene mouse Tcell 937311"
                                                                                                                                                                                                                                                                                                     Score 13.8; DB 163; Length
Pred. No. 2.7e+03;
3; Mismatches 0; Indels
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MEDLINE 97044477 COMMENT Contact: Chin, H National Institute of Mental Health 6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD 20892-9643, USA	Tel: 301 443 1706 Fax: 301 443 9890 Email: mEsr@mail.nih.gov Coligo-dT track not found, Not I site shown in beginning of sequence is likely internal to the message. cDNA Library Preparation: M.B. Soares Lab Clone distribution: Researchers may obtain BMAP cDNA clones from RESEARCH GENETICS. It should be noted that Bento Soares is generating a small number of addittional specialized non-redundant arrays of BMAP cDNAs whose availability will be considered under appropriate and limited collaborative arrangements by Value of Markey and Inmited collaborative arrangements	FEATURES Location/Qualifiers source /organism="Mus musculus" /strain="C57BL/64" /db_xref="taxon:10090" /clone="U1" + BZ1-blp-e-08-0-UI" /clone="U1b="NHEMAPP.MHIZ_S1" /dev_stage="?7-32 days" /lab_host="Vector: pT713D-pac (Pharmacia) with a modified	NTH_BMAP_MHIZ_SI_library is a subtracted library derived from NIH_BMAP_MHIZ_SI_library is a subtracted library derived from nONE hippocompus tissue. For a detailed description of the library from which this clone was 'derived, please visit our web site at brainest.eng.ulowa.edu. TAG_SEO-None found" 38 t ORIGIN	Ouery Match 92.0%; Score 13.8; DB 149; Length 151; Best Local Similarity 80.0%; Pred. No. 2.6e+03; Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0; Qy 1 RCTCCAYTCRCTCA 15 1		ORGANISM Bos taurus Eukaryota; Wetazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Bovinae; Bos. REFERENCE 1 (bases 1 to 173) AUTHORS Smith,T.P.L., Casas,E., Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., Fahrentug,S.C., Freking,B.A., Rohrer,G.A., Laegreid W.W. and Keele,J.W. TITLE Design and use of four pooled tissue normalized cDNA libraries for EST discovery in cattle JOURNAL Unpublished (2000) COMMENT Contact: Smith TPL	Soba, was, us meet Animal Research Center, PO Box 166, Clay Center, NE 68933-0166, USA Tel: 402 762 4366 Fax: 402 762 4390 Email: smith@email.marc.usda.gov
SUMMARIES . Description	458328 BF458328 UI-M-BZ1- 601412 BF601415 266391 MA BC076128 MR2-BT059 505954 A1505954 v121f12.x 5548570 CITB1-E1- 8051868 BB051868 AMAH7497 A54258 MAR A2009 A5562009 v121904.r BB024272 BB024272 AF061117 AF061117 BB038288 BB03888	3 BB024897 BB0272 SB47801 T AA083143 AA083143 AA083143 AA08143 AA08143 AA083143 AA08143 AA083143 AA0821043 AA083143 AA0817922 SF277 WAR	106268 AV406268 AV406268 AV406268 AV406268 AV406268 AV40625_D AV401401 AV406101 AV40	·	8	EST 01-DEC-20 LBMAP_MHI2_S1 Mus musculus cDN NNA sequence. Craniata; Vertebrata; Euteleo	oares,M.B. : two approaches to fac 196)
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

em_gss_rod8: gb_gss35:* gb_gss36:* gb_gss37:*

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The IL-13 binding protein and related therapeutic molecules can be used in the antagonism of at least one IL-13 activity. They can be used for treating IL-13 mediated conditions such as certain allergic conditions such as asthma or to inactivate locally administered IL-13 after IL-13 treatment. The products can also be used as diagnostic agents, e.g. for detecting autoimmune diseases. The antibodies can also be used for immunotherapy and may also be used as a diagnostic tool.
                                                 Claim 10; Page 46; 69pp; English.
  for diagnosis or detection
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Gaps ; 0 Score 13.8; DB 19; Length 465; Pred. No. 1.8e+02; 3; Mismatches 0; Indels 0; Query Match 92.0%; Best Local Similarity 80.0%; Matches 12; Conservative 1 RCICCAYICRCICCA 15 g ò

Sequence 465 BP; 158 A; 79 C; 92 G; 135 T; 1 other;

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Search completed: August 29, 2001, 20:16:40 Job time: 7421 sec

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uncl8-1, vamp3, snap-23, and the rab family of proteins.
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                                                                                                                                                                                                                                                                                                                       Exocytosis pathway protein; Exo protein; antiparkinsonian; antidiabetic; antiallergic; antiasthmatic; nootropic; neuroprotective; anticonvulsant; vulnerary; asthma; inflammation; allergy; Chediak-Higashi syndrome; CHS; Alzheimer's disease; Parkinson's disease; Huntington's disease; diabetes; digestion disorder; wound healing disorder; gene therapy; ss.
                       S
                  haemopoletin receptor protein family NR8 gene. The sequence was used to isolate further mouse NR8 genes. Antibodies to the NR8 family proteins are used for the diagnosis of blood formation disorders. Compounds identified as binding to the proteins are used for the treatment of
                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New nucleic acids encoding Exo proteins which are useful in the diagnosis, treatment or prevention of exocytosis-mediated disorders such as asthma, inflammation and allergies
           sequence represents a PCR amplified fragment of the mouse
                                                                                                                                        0;
                                                                                                                    Length 330;
                                                                                                                                         Indels
                                                                                                              Score 13.8; DB 21;
Pred. No. 1.8e+02;
3. Mismatches 0;
                                                                                   Sequence 330 BP; 72 A; 96 C; 94 G; 68 T; 0 other;
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                                                                                                                                        3; Mismatches
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/product= "IL-13 binding protein Open Reading Frame 1"
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sequence."
Exoproteins and their agonists and antagonists are useful in the diagnosis, treatment or prevention of exocytosis-mediated disorders such as asthma, inflammation, allergies, Chediak-Higashi Syndrome (CHS), Alzheimer's disease, Parkinson's disease, Huntington's disease, diabetes, digestion disorders and wound healing disorders. The nucleic acids, antagonists or agonists of Exo proteins are useful in gene therapy. The nucleic acids are also useful for generating transgenic or knock-out animals which can be used in the development and screening of therapeutically useful reagents.
                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Therapeutic, IL-3 mediated condition; allergy; asthma; diagnosis; autoimmune disease; antibody; immunotherapy; ss.
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                                                                                                                                                                                                                                                                                                                                                               Length 444;
                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Interleukin-13 binding protein C-terminal region gene.
                                                                                                                                                                                                                                                                                  Sequence 444 BP; 124 A; 115 C; 115 G; 87 T; 3 other;
                                                                                                                                                                                                                                                                                                                                                               Score 13.8; DB 21;
Pred. No. 1.8e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                        3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1998-207062/18.
P-PSDB; AAW56255, AAW56257.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
1..465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sednence."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAV22698 standard; DNA; 465 BP.
                                                                                                                                                                                                                                                                                                                                                               92.0%;
80.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97WO-AU00591.
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Best Local Similarity 80.0
Matches 12; Conservative
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/*tag=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     expressed sequence tags (EST's) and are used in a 3' RACE (rapid expressed sequence tags (EST's) and are used in a 3' RACE (rapid amplification of CDNA ends) reaction to amplify the novel ligand-binding receptor, Zcytor2, from humans and macaques. Zcytor2 is a receptor for cytokines (particularly interleukin-13) expressed on the surface of testicular cells, probably being involved in spermatogenesis. It can be used to detect ligands that promote proliferation and/or differentiation of such cells in cultures and may also be used to treat infertility.

Antagonists of this receptor may be used to characterise ligand-receptor interactions and as male-specific contraceptives. By blocking the action of IL-13, receptor antagonists and ligand-binding this receptor can also be used to modulate immune function, e.g. in allergy and asthma, as a diagnostic to determine circulating levels of ligand and also to isolate and purify ligands. Antibodies can be used to assay circulating receptor (an abnormal level may be indicative of disease such as cancer), for labelling cells that express the receptor, and therapeutically as
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; secreted Klotho/Ig heavy chain constant region chimeric protein; immunoglobulin G4; gene therapy; antibody; antiarthritic; nephrotropic; kidney disease; oedema; dropsy; arthritis; IgG1 heavy chain; hinge; CH2 domain; IL-5R alpha chain; interleukin-5 receptor; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human IL-5R alpha chain-IgG4 hinge/CH2 domain PCR primer, SEQ ID NO:15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                       New nucleic acid encoding testis-specific cytokine receptor - useful for identification of ligands or antagonists, potentially for use as male contraceptives or for infertility treatment
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                            Grant FJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 92.0%; Score 13.8; DB 18;
80.0%; Pred. No. 1.5e+02;
ive 3; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 25 BP; 6 A; 1 C; 11 G; 7 T; 0 other;
                                                           Foster DC,
                                                                                                                                                                         Example 1; Page 59; 79pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAA61554 standard; DNA; 71 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99WO-JP06152
                                                            Baumgartner JW, Farrah TM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-OCT-2000 (first entry)
                                   (ZYMO ) ZYMOGENETICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best_Local Similarity 80.0
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 RCTCCAYTCRCTCCA 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22 ACTCCACTCACTCCA
                                                                                               WPI; 1997-470820/43
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-NOV-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                     antagonist.
                                                                        O'Hara PJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAA61554;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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The invention relates to chimeric proteins comprising the human Klotho protein fused to a human immunoglobulin (ABB1691-B11694), and to DNA sequences encoding them (AAA61542-A61545). It also relates to gene therapy vectors comprising DNA encoding the chimeric proteins of the invention, to detection and assay of molecules which interact with Klotho, to antibodies raised against the chimeric protein and to a diagnostic method for Klotho-related disorders using the antibodies. The chimeric proteins of the invention have antiarthritic and nephrotropic activity, and may be used for the treatment, prevention and diagnosis of disorders with which Klotho is associated, including kidney disease, oedema (dropsy) and arthritis. Sequences AAA61557 represent PCR primers used in an exemplification of the invention to generate and amplify DNA encoding the human IL-5 receptor (interleukin-5 receptor) alpha chain and the hinge and part of the CH2 domain of the human IgG4 (immunoglobulin G4) heavy chain.
                                                                                                                          Chimeric polypeptide containing klotho protein bound to an immunoglobulin for treatment and prevention of kidney disease, dropsy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 13.8; DB 21;
Pred. No. 1.6e+02;
3; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 71 BP; 16 A; 13 C; 25 G; 17 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fragment of mouse NRB sequence used as a probe.
Kato Y, Nabeshima Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 7; Page 172-173; 176pp; Japanese
                                                                                                                                                                                                                                                         Example 1; Page 89; 94pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92.0%;
80.0%;
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98JP-0297409
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Best Local Similarity 80.0
Matches 12; Conservative
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   Nakamura K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          formation disorders -
                                                               WPI; 2000-376499/32.
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                                                                                                                                                                                         and arthritis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9967290-A1.
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19-OCT-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAZ59255;
   Hanai N,
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Synthetic.
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                                                                                                                                                                                                                                                                                                         The probe AAV27166 and primers AAV27167-V27168 were used in a method of the invention to isolate NR6 a novel haemopoietin receptor (HR). Interaction between the novel HR and a ligand facilitates proliferation, differentiation and survival of a wide variety of cells. The HR and it's derivatives can be used for modulating the activity of the receptors e.g. to regulate development, maintenance or regeneration in an array of different cells and tissues in vitro and in vivo. They can be present in therapeutics used for modulating neuronal proliferation, differentiation and survival. The products can also be used for detection and diagnosis, e.g. for cancers or predisposition to cancers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; variant thrombospondin 1; variant thrombospondin 4; SNP; polymorphism; vascular disease; coronary artery disease; forensics; myocardial infarction; atherosclerosis; stroke; venous thromboembolism; pulmonary embolism; paternity test; ds.
cell survival; therapeutic; neuronal proliferation; drug screening; ss;
PCR; primer; amplification; Human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                             New isolated haemopoletin receptor - used for developing products for modulating proliferation, differentiation and survival of cells, e.g. neuronal cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 13.8; DB 19; Length 18; Pred. No. 1.4e+02; 3; Mismatches 0; Indels
                                                                                                                                                                                Alexander W, Fabri L, Farley A, Hilton DJ, Kikuchi Y;
Kojima T, Maeda M, Nash A, Nicola NA, Rakar S, Willson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human gene single nucleotide polymorphism #721.
                                                                                                                                                                                                                                                                                                                                                                                                                                      BP; 3 A; 8 C; 4 G; 3 T; 0 other;
                                                                                                                                                                                                                                                                                        Example 16; Page 66; 182pp; English.
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replace(11,T)
/*tag= a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     92.0%;
80.0%;
                                                                                                                                                   OPERATIONS PTY
                                                                                                                              96AU-0002246
                                                                                                         97WO-GB02479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAF95960 standard; DNA; 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                   (AMRA-) AMRAD OPERATIONS
(DZIE/) DZIEGLEWSKA H E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 RCTCCAYTCRCTCCA 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1998-260970/23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 12; Conserv
                                Synthetic.
Homo sapiens.
                                                                                                                             11-SEP-1996;
                                                               WO9811225-A2
                                                                                                         11-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 18
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                                                                                    19-MAR-1998
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Variation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAF95960;
                                                                                                                                                                                                    Zhang J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 10
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The present invention provides a method of diagnosing a vascular disease in an individual, involving determining the sequence at various polymorphic sites within the human thrombospondin 1 and thrombospondin 4 genes. The sequences at a number of polymorphic sites are also provided in the specification. In particular, the method can be used in the diagnosis of atherosclerosis, myocardial infarction, coronary heart disease, stroke, peripheral vascular diseases, venous thromboembolism and pulmonary embolism. Single nucleotide polymorphisms (SNPs) are also useful in forensize, patentity testing, genetic analysis and phenotype correlations to diseases. The present sequence is an example of one of the human gene SNPS shown in the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               McCarthy JJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     applications such as forensics, paternity testing, medicine, genetic analysis and phenotype correlations to diseases such as diabetes and atherosclerosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cytokine receptor; ligand binding; testicular cell; spermatogenesis; infertility; antagonist; contraceptive; diagnostic; therapeutic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acids comprising single nucleotide polymorphisms, useful in
/standard_name= "single nucleotide polymorphism"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Daley GQ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   92.0%; Score 13.8; DB 22;
80.0%; Pred. No. 1.4e+02;
iive 3; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 21 BP; 4 A; 2 C; 11 G; 4 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lander ES, Gargill M, Ireland JS, Bolk S,
                                                                                                                                                                                                                                                                                                                                                                                            (WHED ) WHITEHEAD INST BIOMEDICAL RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Examples; Page 98; 242pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAT96787 standard; cDNA; 25 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                  (MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                                                                                                                                             26-JUL-2000; 2000US-0220947.
16-AUG-2000; 2000US-0225724.
                                                                                                                                                                                              07-SEP-2000; 2000WO-US24503
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Best Local Similarity 80.0
Matches 12; Conservative
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haemopoietin receptor protein family NR8 genes. The NR8 family sequences were initially searched for comparison on a nucleic acid database with the nucleic acid probe sequence TGGAGYNNYTGGAGY encoding the amino acid sequence Trp-Ser. Tha artip-Ser. The sequences AAZ59258-259300 and AAZ90816-290925 represent specific examples of probe sequences used in the search. Antibodies to the NR8 family proteins are used for the diagnosis of blood formation disorders. Compounds identified as binding to the proteins are used for the treatment of such disorders.
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                                                                                                                                                                                  Gaps
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                                                                                                                                                   92.0%; Score 13.8; DB 21;
80.0%; Pred. No. 1.4e+02;
1ive 3; Mismatches 0;
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                                                                                                                 Sequence 15 BP; 3 A; 0 C; 8 G; 4 T; 0 other;
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98JP-0297409
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Best Local Similarity
Matches 12; Conserv
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19-OCT-1998;
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haemopoietin receptor protein family NR8 genes. The NR8 family sequences were initially searched for comparison on a nucleic acid database with the nucleic acid probe sequence TGGAGYNNYTGGAG encoding the amino acid sequence TFP-Ser. The sequences AAZ59258-Z59300 and AAZ90816-Z90925 represent specific examples of probe sequences used in the search. Antibodies to the NR8 family proteins are used for the diagnosis of blood formation disorders. Compounds identified as binding to the proteins are used for the treatment of such disorders.
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80.0%;
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ID AAZ90894 standard; DNA; 16
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                                                                                                                                                                                                                                                                             Human NR8 gene probe #122
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Best Local Similarity 80.0'
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19-OCT-1998;
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92.0%; Score 13.8; DB 21; Length 15; 80.0%; Pred. No. 1.4e+02;

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Best Local Similarity Matches 12; Conserv

Query Match

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AAZ90848;

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The invention relates to the isolation of sequences encoding human haemopoletin receptor protein family NR8 genes. The NR8 family sequences were initially searched for comparison on a nucleic acid database with the nucleic acid probe sequence TGGAGYNNNTGAGY encoding the amino acid sequence Trp-Ser-Xaa-Trp-Ser. The sequences AAZS9258-229300 and AAZ90816-290925 represent specific examples of probe sequences used in the search. Antibodies to the NR8 family proteins are used for the diagnosis of blood formation disorders. Compounds identified as binding to the proteins are used for the treatment of such disorders.
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Pred. No. 1.4e+02;
3; Mismatches 0;
                                                                      (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
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80.0%;
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ID AAZ90880 standard; DNA; 15
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Best Local Similarity 80.0
Matches 12; Conservative
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                                                                                                             Maeda M;
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               24-JUN-1998;
19-OCT-1998;
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                                                                                                         Haemopoletin receptor family; NR8; antibody; diagnosis; blood formation disorder; fusion protein; probe; ss.
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                                   (first entry)
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                                                                      Human NR8 gene probe #76.
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Matches 12; Conserv
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Sequence 15 BP; 2 A; 7 C; 0 G; 3 T; 3 other;
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Best Local Similarity 80.0
Matches 12; Conservative
                                                                        Query Match 92.0
Best Local Similarity 100.
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human NR8 gene probe #58
                                                                                                                                                                 1 RCTCCAYTCRCTCCA 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-JUN-1999;
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ID AAZ908
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                                                                                                                                                                                                                                                                                  RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                molecules encoding a novel heamopoietin receptor (HR). Interaction between the novel HR and a ligand facilitates proliferation, differentiation and survival of a wide variety of cells. The HR and it's derivatives can be used for modulating the activity of the receptors e.g. to regulate development, maintenance or regeneration in an array of different cells and tissues in vitro and in vivo. They can be present in therapeutics used for modulating neuronal proliferation, differentiation and survival. The products can also be used for detection and diagnosis, e.g. for cancers or predisposition to cancers, or for drug screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Haemopoietin receptor; cell proliferation; cell differentiation; cancer;
cell survival; therapeutic; neuronal proliferation; drug screening; ss;
                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated haemopoletin receptor - used for developing products for modulating proliferation, differentiation and survival of cells, e.g. neuronal cells
                                                                 conserved motif (AAR92812) found in haemopoieth receptors. The probes are used in the identification and/or cloning of genes coding for novel haemopoieth receptors, e.g. the murine interleukin-11 (IL-11) receptor alpha chain gene (AAT17868). Such receptors are defined by their ability to hybridise to the probes under medium stringency conditions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 probes AAV27138 and AAV27139 are used to identify nucleic acid
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                                                                                                                                                                                                                                                                                                        Length 15;
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Maeda M, Nash A, Nicola NA, Rakar S, Wills
                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                   Score 13.8; DB 17;
Pred. No. 1.4e+02;
                                                                                                                                                                                                                                Sequence 15 BP; 2 A; 7 C; 0 G; 3 T; 3 other;
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Claim 12; Page 51; 87pp; English.
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                                                                                                                                                                                                                                                                                                 92.0%; Sccilarity 100.0%; Pr
Conservative 0;
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                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 15; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAV27139;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to the isolation of sequences encoding human haemopoletin receptor protein family NR8 genes. The NR8 family agequences were initially yearched for comparison on a nucleic acid database with the nucleic acid probe sequence TGGAGYNNNTGAGY encoding the amino acid sequence Trp-Ser-Xaa-Trp-Ser. The sequences AAZS9258-2S9300 and AAZ90816-290925 represent specific examples of probe sequences used in the search. Antibodies to the NR8 family proteins are used for the diagnosis of blood formation disorders. Compounds identified as binding to the proteins are used for the treatment of such disorders.
                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hemopoletin receptor protein family \ensuremath{\mathsf{NRR}} used for diagnosis of blood formation disorders -
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                    Length 15;
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                                                                           Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Haemopoietin receptor family; NR8; antibody; diagnosis; blood formation disorder; fusion protein; probe; ss.
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Pred. No. 1.4e+02;
3; Mismatches 0;
                 Score 13.8; DB 19;
Pred. No. 1.4e+02;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1; Page 40; 176pp; Japanese.
92.0%; Scor.
100.0%; Pre
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80.0%;
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98JP-0297409
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gene pro
gene pro
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Human gene single
Human and macaque
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                                                                                               August 29, 2001, 18:12:59; Search time 301.32 Seconds (without alignments) 31.258 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene
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| SIDS8/goddata/geneseq/geneseqn/NML991.DAT:
| SIDS8/goddata/geneseq/geneseqn/NML992.DAT:
| SIDS8/goddata/geneseq/geneseqn/NML993.DAT:
| SIDS8/goddata/geneseq/geneseqn/NML995.DAT:
| SIDS8/goddata/geneseq/geneseqn/NML995.DAT:
| SIDS8/goddata/geneseq/geneseqn/NML995.DAT:
| SIDS8/goddata/geneseq/geneseqn/NML998.DAT:
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| SIDS8/goddata/geneseq/geneseqn/NML9000.DAT:
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/SIDS8/gcgdata/geneseq/geneseqn/NA1981.DAT:*
/SIDS8/gcgdata/geneseq/geneseqn/NA1982.DAT:*
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                       730101 seqs, 313950809 residues
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Maximum Match 100%
Listing first 45 summaries
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AAZ90893
AAZ90894
AAV27168
AAF95960
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AAZ90830
                                                                       OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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Match Length
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	ບ	12	13.	ω	٠.	71	21	AAA61554	Human IL-5R alpha
	ပ	13	13.	œ		330	21	AAZ59255	Fragment of mouse
_	ပ	14	13.	æ		444	21	AAA89731	Mouse IL-3 recepto
	ပ	15	13.	80	92.0	465	19	AAV22698	Interleukin-13 bin
	U	16	13.	8	٠.	657	21	AAZ94555	Cytokine receptor
	U	17	m	æ	92.0	069	16	AAT04952	Interleukin 4 comp
	ပ	18	13.	8		693	15	AA054831	
	O	19	13.	8	92.0	969	18	AAV04437	
	ပ	20	3	8		759	1.5	AAQ54830	
		21	m	8		807	1.0	AAN90793	
	O	22	3	8		870	21	AA250746	
	ပ	23	m	8		907	21	AA259253	Human NR8gamma 3'
	υ	24	m	æ		931	21	AAF20982	Human low adenosin
	ပ	25	13.	8		931	21	AAA34860	Human adenosine re
	υ	56	13.	8		938	19	AAV27142	Novel haemopoietin
	ပ	27	3	8		938	21	AAA46793	DNA encoding a mur
	O	28	13.	8		947	19	AAV22702	Mature interleukin
	ပ	59	13.	8		975	21	AAA70701	Human interleukin
	ပ	30	13.	8		1035	21	AAZ40288	SR345 coding seque
	O	31	13.	8		1044	15	AAQ54829	IL-2 receptor gamm
	ပ	32	3	8		1074	18	AAV04440	Interleukin 6 rece
	ပ	33	3	8		1079	19	AAV22701	Construct containi
	ပ	34	13.	8		1126	18	AAT96784	Celebus macaque 2c
	υ	35	m	89		1128	21	AAZ59247	Human NR8alpha/TPO
	O	36	m	80		1167	18	AAT96783	Human 2cytor2 cyto
	ပ	37	13.	8		1188	13	AAQ22974	Sequence of the op
	ပ	38	13.	8		1218	20	AA206347 .	Nucleotide sequenc
	ပ	39	3	8		1218	21	AA250346	Mouse orphan cytok
	O	40	13.	æ		1229	21	AAZ94577	
	υ	4.1	13.	8		1233	20	AA208861	Human DNAX soluble
	ပ	42	13.	8		1260	13	AAQ22972	Sequence encoding
	O	43	13.	8		1260	20	AAZ09202	Human IL-6 recepto
	O	44	13.	8		1281	20	AAX89654	cDNA encoding a hu
	O	45	13.	8		1288	19	AAV04131	Human HR-1 recepto
								ALIGNMENTS	
	RES	RESULT	-						
	<u>:</u> :::::::::::::::::::::::::::::::::::	AAT1	AAT17870		standard;	: DNA;	15 E	BP.	
	X X	AAT1	AAT17870	٠.					
	××								
	DŢ	21 - M	21-MAY-1996	966	(fire	(first entry)	(Y.		

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RABIOLIT 1
AAT17870
ID AAT17870 standard; DNA; 15 BP.

XX
AC AAT17870;
XX
AC AAT17870;
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DT 21-MAY-1996 (first entry)
XX

W Haemopoietin receptor probe HVB1.
XX

W Haemopoietin; interleukin-11; IL-11; receptor; agonist; antagonist;
XX

XX

Synthetic.
XX

DD 14-MAR-1996.
XX

ED 14-MAR-1996.
XX

PR 05-SEP-1994; 94AU-0007902.
XX

PR 05-SEP-1994; 94AU-0007901.
XX

PR 05-SEP-1994; 95AU-0007901.
XX

PR 05-SEP-1994;
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Search completed: August 29, 2001, 19:51:58 Job time: 17236 sec

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Gaps

; 0

Indels

Length 1218;

19 others

us-09-532-263-7.rge

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Submitted (13-DEC-2000) Department of Plant Pathology & Microbiology, Texas A&M University, 2132 TAMUS, College Station, TX 77843-2132, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Stachybotrys chartarum.
Stachybotrys chartarum
Eukaryota; Fungi; Ascomycota; mitosporic Ascomycota; Stachybotrys.
I (bases 1 to 1227)
Peplow, A.W. and Beremand, M.N.
Putative trichothecene genes of Stachybotrys chartarum
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                   AF329103 1227 bp DNA PLN 29-JAN-2001
Stachybotrys chartarum trichodiene synthase (TRI5) gene, complete
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326 c 316 g 264 t
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Pred. No. 8.6e+02;
3; Mismatches 0;
                                                                                                                                                 91;
                                                                                                                                              Score 13.8; DB 91
Pred. No. 8.6e+02;
3; Mismatches 0
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<1. .>1227
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join(<1. .469,545. .>1227)
/gene="TRI5"
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join(1. .469,545. .1227)
/gene="TRI5"
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Peplow, A.W. and Beremand, M.N.
Direct Submission
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1. .1227
                                                  223
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AF329103.1 GI:12584944
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/gene="LEPR"
                                                                                                                                              92.0%;
80.0%;
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80.0%;
                         /number=8
                                                                                                                             Query Match
Best Local Similarity 80.0'
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Best Local Similarity 80.0
Matches 12; Conservative
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669 ACTCCAGTCACTCCA 655
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DEFINITION
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AF329103/c
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/db_xref="G1:1151069"
/db_xref="G1:115106
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                Direct Submission
Submitted (15-JUN-1995) Nancy Y. Ip, Department of Biology, The
Hong Kong University of Science and Technology, Clear Water Bay,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
Submitted (24-MAY-1996) Clinical Diabetes and Nutrition Section,
National Institutes of Health, 4212 N. 16th Street, Phoenix, AZ
85016, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Thompson.D.B., Ossowski,V., Sutherland,J., Apel,W. and Biesterfeildt,J.
Human Leptin Receptor
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 (bases 1 to 1218)
Thompson, D.B., Ossowski, V., Sutherland, J., Apel, W. and
Biesterfeldt, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 13.8; DB 8; Length 1089;
Pred. No. 8.6e+02;
3; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                     /note="CNTF receptor alpha component"
/codon_start=1
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8.
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Human leptin receptor (LEPR) gene, exon
U59253.1 GI:1589760
                    J. Neurochem. 65 (6), 2393-2400 (1995) 96064819
                                                                                                                                                                                                                                                          /organism="Gallus gallus"
/db_xref="taxon:9031"
/tissue_type="brain"
/dev.stage="embryo"
1. 1089
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/db_xref="taxon:9606"
/chromosome="1"
/map="1p31"
550. 694
                                                                                                                                                                                                               Location/Qualifiers
1. .1089
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  denervated skeletal muscle
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80.0%;
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Ip, N.Y.
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Best Local Similarity 80.0
Matches 12; Conservative
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Gaps

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Indels

Length 1227;

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cDNA encoding Ig-CRH region of human G-CSF receptor.
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/db_xref="taxon:9606"
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80.0%;
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U29245
U29245.1 GI:1151068
                                                                                                                                                                                                                                                                                C12R1:91),
(C12P21/02,C12R1:91);
                                                                                                                                                                                                                                                                                                       strandedness: Double;
topology: Linear;
                                                                                                                                                                                                       no sapiens (human)
1996140678-A/2
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Best Local Similarity 80.0
Matches 12; Conservative
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anti-sense: No;
                                                    Homo sapiens (human)
                           JP 1996140678-A/2.
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   δ
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join(L38020.1:1. .152,L38021.1:21. .132,L38022.1:26. .110,
L38023.1:26. .259,L38024.1:26. .144,L38024.1:319. .484,
L38024.1:1595. .1758,26. .206,551. .719,809. .993)
/product="ciliary neurotrophic factor alpha receptor"
join(L38022.1:26. .110,L38023.1:26. .259,L38024.1:26. .144,
L38024.1:319. .484,L38024.1:1595. .1758,26. .206,551. .719,
                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 993)
Valenzuela,D.M., Rojas,E., Le Beau,M.M., Espinosa,R., Brannan,C.I., McClain,J., Masiakowski,P., Ip,N.Y., Copeland,N.G., Jenkins,N.A. and Yancopoulos,G.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LHVGLPPREPVLSCRSNTYPKGFYCSWHLPTPTYIPNTVVLHGSKIMVCEKDPAL
KNRCHIRYMHLFSTIKYKVSISVSNALGHNATAITFDEFTIVKPDPENVVARPVPSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRRLEVTWQTPSTWPDPESFPLKFFLRYRPLILDQWQHVELSDGTAHTITDAYAGKEY
IIQVAAKDNEIGTWSDWSVAAHATPWTEEPRHLTTEAQAAETTTSTTSSLAPPPTTKI
CDPGELGSGGGPSAPFLVSVPITLALAAAAATASSLLI"
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                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="MAAPVPWACCAVLAAAAAVVYAQRHSPQEAPHVQYERLGSDVTL
PCGTANWDAAVTWRVNGTDLAPDLLNGSQLVLHGLELGHSGLYACFHRDSWHLRHQVL
                                                                                                                                                         Genomic organization and chromosomal localization of the human and mouse genes encoding the alpha receptor component for ciliary deurotrophic factor Genomics 25 (1), 157-163 (1995) 95293367
                                                                                                                                                                                                                                                                                                                                                                                           /codon_start=1
/product="cillary neurotrophic factor alpha receptor"
/protein_id="AAA9137.1"
/db_xref="GI:608656"
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8-10, complete cds.
L38025.
L38025.1 GI:608654
cillary neurotrophic factor alpha receptor.
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Pred. No. 8.5e+02;
3; Mismatches 0;
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Last updated, Version 2)

    10. 1993
    /organism="Homo sapiens" /db_xref="taxon:9606"
    /chromosome="9"

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/note="non-coding exon"
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80.0%;
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a 336 c
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809. .993
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Matches 12; Conservative
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139 GCTCCAGTCACTCCA 125
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65,
                                                                            Homo sapiens
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                                                   6 of 6
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E11420/c
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AC E11420;
XX
XX
XX E11420.1
XX
DT 08-OCT-1
XX
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                                                                        ORGANISM
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                         Ota Y., Hiraoka O., Anaguchi H.;
"DNA CODING FOR PROTEIN OF LIGAND-BONDING REGION CONTAINING CRH REGION OF
GRANULOCYTE COLONY STIMULATING PACTOR RECEPTOR";
Patent number JP1996140678-A/2, 04-JUN-1996.
TANPAKU KOGAKU KENKYUSHO:KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gallus gallus ciliary neurotrophic factor receptor alpha component
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.

(bases 1 to 1089)

1 (bases 1 to 1089)

Cloning of the alpha component of the chick ciliary neurotrophic factor receptor: developmental expression and down-regulation in
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                                                                                                                                                                                                                                                                                                                                                                             04-JUN-1996
15-NOV-1994 JP 1994280655
OTA YOSHIMI, HIRAOKA OSAMU, ANAGUCHI HIROYUKI
C12N15/09,C07H21/04,C07K14/715,C12N5/10,C12P21/02,(C12N5/10,
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Pred. No. 8.5e+02;
3; Mismatches 0;
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Gaps

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RESULT 11
HUMCNFARNG6/c
LOCUS HUMCNFAR06 993 bp DNA PRI 09-JAN-2001
DEFINITION Homo'sapiens ciliary neurotrophic factor alpha receptor gene, exons
                                                                                                                                                                                                                                                                                                                                            Bukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 801)

Chua S.C., Chung W.K., Wu-Peng,X.S., Zhang,Y., Liu,S.M., Tartaglia,L. and Leibel,R.L. Phenotypes of mouse diabetes and rat fatty due to mutations in the OB (leptin) receptor Science 271 (5251), 994-996 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (22-DEC-1997) Pediatrics, Columbia University, 1150 St. Nicholas Avenue, New York, NY 10032, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chases 1 to 801)
Chua, S.C., Koutras, I.K., Han, L., Liu, S.M., Kay, J., Young, S.J.,
Chung, W.K. and Leibel, R.L.
Fine structure of the murine leptin receptor gene: splice site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 (bases 1 to 801)
Chua,S.C., Koutras, I.K., Han, L., Liu,S.M., Kay,J., Young,S.J.,
Chung,W.K. and Leibel,R.L.
                                                                                                                                                                                                                                09-JAN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      suppression is required to form two alternatively spliced
                                                                    Length 639;
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                            Sequence 639 BP; 135 A; 227 C; 174 G; 103 T; 0 other;
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                                                                    Score 13.8; DB 45;
Pred. No. 8.3e+02;
3; Mismatches 0;
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Pred. No. 8.4e+02;
3; Mismatches 0;
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 /organism="Homo sapiens"
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/chromosome="4"
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Genomics 45 (2), 264-270 (1997)
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                                                                    Query Match 92.0%;
Best Local Similarity 80.0%;
Matches 12; Conservative
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80.0%;
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Best Local Similarity 80.0
Matches 12; Conservative
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606 GCTCCAGTCGCTCCA 592
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419 ACTCCAGTCACTCCA 405
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MUMULEPR06/c
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Ota Y., Anaguchi H.;
Ota Y., Anaguchi H.;
"Und CODING PROTEIN EC IN LIGAND-BOUND REGION IN GRANULOCYTE COLONY
STIMULATING FACTOR RECEPTOR";
Patent number JP1996131172-A/2, 28-MAY-1996.
TANPAKU KOGAKU KENKYUSHO:KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="CRH region of human G-CSF receptor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTA YOSHIMI, ANAGUCHI HIROYUKI
C12N15/09,C07H21/04,C07K14/715,C12N1/21,C12P21/02,(C12N1/21,
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    639
    /note="CRH region of G-CSF receptor"

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                                                                                                                              BP; 135 A; 227 C; 174 G; 103 T; 0 other;
                                                                                                                                                                      Score 13.8; DB 45;
Pred. No. 8.3e+02;
3; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               cDNA encoding CRH region of human G-CSF receptor
                                                                                                                                                                                                                                                                                                                                                                                                                   07-OCT-1997 (Rel. 52, Created)
02-SEP-2000 (Rel. 65, Last updated, Version 2)
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/cell_line="U937"
/tissue_type="placenta"
1. 639
                                                                                 /db_xref="taxon:9606"
/organism="Homo sapiens"
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    .639
    /db_xref="taxon:9606"

                                         Location/Qualifiers
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14-NOV-1994 JP 1994278841
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80.0%;
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:C12P21/02,C12R1:19);
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topology: Linear;
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JP 1996131172-A/2
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Best Local Similarity 80.0
Matches 12; Conservative
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anti-sense: No;
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 misc_feature
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Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                       BAC ends sequenced at TIGR from the RPCII1 BAC library. Designed and developed at the Stanford Human Genome Center.

Location/Qualifiers
1. 620
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JP 1995227288-A/2
29-AuG 1995
30-MAY-1994 JP 1984116252
21-DEC-1993 JP 93P 321862
OTA YOSHIMI, MANGUCHI HIROYUKI, HIRAOKA OSAMU
C12N15/09,C12P21/O2,(C12N15/09,C12R1:91),(C12P21/O2,C12R1:19);
strandedness: Double;
topology: Linear;
hypothetical: No;
anti-sense: No;
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Pred. No. 8.3e+02;
3; Mismatches 0;
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02-SEP-2000 (Rel. 65, Last updated, Version 2)
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/tissue_type="Placenta"
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Patent number JP1995227288-A/2, 29-AUG-1995.
TANPAKU KOGAKU KENKYUSHO:KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cDNA encoding CRH region of G-CSF receptor.
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/db_xref="taxon:9606"
/map="11"
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267. .547
267. .289
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Best Local Similarity
Matches 12; Conserv
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primer_bind
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                  2 (bases 1 to 597)
Coleman, A.W. and Mai, J.C.
Direct Submission
Submitted (15-AUG-1996) BioMed, Brown University, Providence, 02912, USA
On Nov 20, 1997 this sequence version replaced gi:2039187.
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94 degrees C for 30 seconds
60 degrees C for 30 seconds
72 degrees C for 23 seconds
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Perkin Elmer 9700
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Stanford University School of Medicine
Miranda Warsaty School of Medicine
Miranda Warsaty School of Medicine
Faz: (560) 320-5800
Faz: (560) 320-5800
Faz: (550) 320-5800
France (550) 320-5800

                                                                                                                                                                                                                                                      /note="ITS1"
/product="Internal transcribed spacer 1"
200. 358
/product="5.8S ribosomal RNA"
359. .597
/note="ITS2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                /product="internal transcribed spacer 2"
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each 1 uM
each 200 uM
: 0.07 units/ul
5 ul
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Pred. No. 8.2e+02;
3; Mismatches 0;
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Olivier,M. and Cox,D.R.
Unpublished, Olivier, M., Cox, D.R. (2000)
Unpublished (2000)
                                                                                                                                                          1. 597
/oganism="Chlamydomonas incerta"
/strain="SAG7.73"
/db_xref="taxon:51695"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Michael Olivier, David R. Cox
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             dNTPs:
Amplifaq Gold Polymerase:
Total Vol:
                                                                                                                                                                                                                                                                                                                                                                                                  142 g
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Polymerization:
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80.0%;
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G56634.1 GI:6121803
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Best Local Similarity 80.0
Matches 12; Conservative
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399 GCTCCAATCACTCCA 385
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VERSION
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TITLE
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COMMENT
                                       AUTHORS
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G56634/c
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MEDLINE
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Length 620; Indels

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rhesus monkey.
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CIU66950/c
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          E 3 (bases 1 to 373)
S van der Poel.J.J.
S van der Poel.J.J.
Lect Submission
L Submitted (03-MAR-1997) Animal Breeding, Agricultural University Wageningen, Marijikeweg 40, Wageningen 6708 PG, The Netherlands GSDB:S:48171.
[Flatfile retrieved from GSDB Fri Feb 23 09:21:05 2001].
Location/Qualifiers
1. 373
I. 373
I. 373
I. 374
/db_xxef="taxon:9031"
/flssue_type="brain"
/dev_stage="brain"
/dev_stage="brain"
/dote="derived from CDNA library".
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  unc-5=immunoglobulin and thrombospondin type 1 transmembrane
protein (alternatively spliced) [Genorhabditis elegans, variety
Bergerac, Genomic/mRNA, 387 nt, segment 6 of 9].
847165
847165.1 GI:258524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              l (bases 1 to 387)
Leung Hagesteijn.C., Spence,A.M., Stern,B.D., Zhou,Y., Su,M.W.,
Hadgecock,B.M. and Culotti.J.G.
UNC-5, a transmembrane protein with immunoglobulin and
thrombospondin type 1 domains, guides cell and pioneer axon
migrations in C. elegans
Cell 71 (2), 289-299 (1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GenBank staff at the National Library of Medicine created this entry [NCBI glabba 116678] from the original journal article. This sequence comes from Fig. 2.

Location/Qualifiers
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/db_xref="taxon:6239"
/variety="Bergerac"
107 g 90 t
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80.0%; Pred. No. 8e+02;
ive 3; Mismatches 0;
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Caenorhabditis elegans
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74 c 53 g
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Matches 12; Conserv
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Matches 12; Conserv
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MEDLINE
PUBMED
                REFERENCE
                               AUTHORS
                                                             JOURNAL
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                                                                                                                                                                                                                                                                                                                                Direct Submission
Submitted (24-JAN-2000) California Regional Primate Research
Center. University of California-Davis, one Shields Avenue, Davis,
CA 95616, USA
                                                                                                                                    Macaca mulatta
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chlamydomonas incerta
Eukaryota; Viridiplantae, Chlorophyta; Chlorophyceae; Volvocales;
AF227555 457 bp mRNA PRI 01-JUN-2000 Macaca mulatta interleukin-6 signal transducer receptor (IL-6)
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1 (bases 1 to 597)

Mai,J.C. and Coleman,A.W.
The internal transcribed spacer 2 exhibits a common secondary structure in green algae and flowering plants
J. Mol. Evol. 44 (3), 258-271 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:9544"
/cell_type="peripheral blood mononuclear cells"
<1. .>457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                       Cytokine Signal Transduction Genes from Rhesus Macaques
Unpublished
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Pred. No. 8.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note-"membrane glycoprotein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                               Cercopithecinae; Macaca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3;
                                                                          AF227555.1 GI:8132802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="gp130"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /dene="IL-6"
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80.0%;
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                                                                                                                                                                                                               1 (bases 1 to 457)
Arredondo, J.
                                                                                                                                                                                                                                                                                           (bases 1 to 457)
                                    mRNA, partial cds.
AF227555
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Best Local Similarity 80.0
Matches 12; Conservative
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Submitted (07-MRR-2000) E-mail contact: humquery@sanger.ac.uk Marker stSG67529 (Primer A : AAAAGTGAAAGAAGGGAAAGG; Primer B : SATAACCCAACGGATGG; amplimer size : 141 bp) was developed from a single pass sequencing read from H.sapiens flow-sorted chromosome 9-12 random shear fragment, SC9-12pJ10F12. Vector : pUC18 Site :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        chicken.

Gallus gallus

Gallus gallus

Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Archosauria; Aves; Neognathae; Galliformes; Phaslanidae;

Phaslaninae; Gallus.

I (bases 1 to 373)

Ruyter-Spira,C.P., Crooijmans,R.P., Dijkhof,R.J., van Oers,P.A.,

Strijk,J.A., van der Poel,J.J. and Groenen,M.A.

Development and mapping of polymorphic microsatellite markers

Anim. Genet. 27 (4), 229-234 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 (bases 1 to 373)

Withdre Spira,C.P., de Koning,D.J., van der Poel,J.J.,

Crooijmans,R.P., Dijkhof,R.J. and Groenen,M.A.

Developing microsatellite markers from cDNA: a tool for adding
expressed sequence tags to the genetic linkage map of the chicken
Anim. Genet. 29 (2), 85-90 (1998)
                                                                                                                                                   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                      NA STS 07-MAR-2000 shear fragment, sequence tagged site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             L48909 373 bp mRNA VRT 23-FEB-2001
Gallus gallus clone cDNA42R microsatellite MCW111 sequence.
L48909
                                                                                                                                                                                                                                                                                                                        Further information : http://www.sanger.ac.uk/HGP/Chr10/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  92.0%; Score 13.8; DB 54; Length 340;
80.0%; Pred. No. 7.9e+02;
live 3; Mismatches 0; Indels 0
                                                                                                                                                                                   1 (bases 1 to 340)
Hunt, S., Sims, S., Willey, D., Carter, N. and Ross, M.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                             /clone="SC9-12pJ10F12"
/tissue_type="Lymphoblastoid cell line"
/clone_lib="SC9-12pJ" 87 t 1 0+++-
                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="10"
                                                         HSJ10F12 340 bp DN
STS from H.sapiens random
AL159451
                                                                                                             AL159451.1 GI:7210385
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                                                                                                                                                                                                                                                                                                                                                                                                        /sex="male
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12; Conservative
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  1 RCTCCARTCRCTCCA 15
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48 GCTCCAGTCACTCCA 34
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                                                                                                                                          human.
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VERSION
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             AF039448 Mus muscu
L38025 Homo sapien
E11420 cDNA encodi
U29245 Gallus gall
U59253 Human lepti
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AF053926 Stachybot
M73238 Human cilia
                                                                                               Z48168 G.gallus mR
S54212 ciliary neu
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I50845 Sequence 2
                                                                                                                                                                                                                                                                              AB015706 Homo sapi
AF068615 Mus muscu
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BC005707 Mus muscu
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D17444 Mouse mRNA
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I56052 Sequence 1
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AR019619 Sequence
AR070271 Sequence
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                                                                                                                                                                                                                                     U09028 Oryctolagus
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AJ308426 Bos tauru
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AR070290 Sequence
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Nicola,N.A., Fabri,L., Farley,A., Nash,A., Willson,T., Rakar,S.,
Zhang,J., Alexander,W., Hilton,D.J., Kojima,T., Maeda,M. and
Kikuchi,Y.
                                                                                                                                                                                                                                                                                                           Sequence 1
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/organism="unidentified"
/db_xref="taxon:32644"
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RESULT A70377

SOURCE

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Gaps

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                                                                                 August 29, 2001, 19:51:55; Search time 1774.1 Seconds (without alignments) 130.780 Million cell updates/sec
                                                                                                                                                                                                                                                  2688314
         GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                        1344157 seqs, 7733874588 residues
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Maximum Match 100%
Listing first 45 summaries
                                                         OM nucleic - nucleic search, using sw model
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A70377 Sequence 7
AL159451 STS from
L48909 Gallus gall
S47165 unc-5-immun
AF227555 Macaca mu
U66950 Chlamydomon
G56634 SHGC-102031
E09857 CDNA encodi

HSJ10F12 L48909 S47134S6 AF227555 CIU66950 G56634 E09857

989 454 54 54

A70377 ΩI

Description

SUMMARIES

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Mechine which results in the intermediate of a continuous source of protein to an animal and stimulate cellular immunity. Such compositions are used to stimulate cellular immunity. Such compositions are used to stimulate cellular immunity (by inducing Th-1 cells or cytotoxic T lymphocytes), particularly as vaccines (live or dead) for treating and preventing diseases caused by intracellular pathogens (bacteria, viruses, rickettsia or protozoa), and also cancer, autoimmune diseases, allergy and bovine spongiform encephalitis, in humans or animals. The waccines are administered by injection, orally and nasally. These compositions provide consistent and long-lasting immunity. Transformed cells used in the method are retained within macrophages, blocking the killing mechanism but producing protective immunogen which is processed and presented by the macrophage. Several immunogens may be included in the same vaccine and the Mycobacterium cells serve as adjuvant.
                                                                                                                                                                                                                                                                                                                                                                                                                This genomic DNA sequence is a fragment of the Mycobacterium fortiutum plasmid pAL 5000 which contains ORF2. This sequence is used in a method which results in the formation of Mycobacterium recombinant
                                                                                                                                                                                                                                                                Recombinant non-pathogenic Mycobacterium as vaccines providing long term cellular immunity - useful against intracellular pathogens, cancer and autoimmune disease, and are retained in host macrophages
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2096 BP; 348 A; 743 C; 670 G; 335 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Fig 6; 120pp; English.
                       98WO-US06056.
                                                                  97US-0042849.
                                                                                                                   (CYTO-) CYTOCLONAL PHARM INC
                                                                                                                                                                                                                     WPI; 1998-568277/48.
                                                                  28-MAR-1997;
                    27-MAR-1998;
                                                                                                                                                                    Labidi AH;
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Search completed: August 29, 2001, 20:16:42 Job time: 7423 sec

1 RCTCCARTCRCTCCA 15

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Gaps

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92.0%; Score 13.8; DB 19; Length 2096; 80.0%; Pred. No. 2e+02; ive 3; Mismatches 0; Indels 0;

Query Match 92.0 Best Local Similarity 80.0 Matches 12; Conservative

Matches

ò 셤 RESULT 13

AAQ83223,

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Vaccine; cellular immunity; Th-1 cell; cancer; cytotoxic T lymphocyte; treatment; prevention; disease; autoimmune; intracellular pathogen; BSE; allergy; bovine spongiform encephalitis; macrophage; immunogen; adjuvant; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A DNA sequence (AAT14602) codes for a novel splice variant (AAR94576) human gpl30. The splice variant was initially detected during the morula to blastocyst transition stage of a human embryo. The splicing event removes the exon coding for the transmembrane domain causing a frameshift resulting in a novel C-terminus (see AAR94575). The splice variant gpl30 antegonises the action of certain growth factors and can be used to ensure correct development of preimplantation embryos, partic. for in vitro fertilisation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        New splice variant of gpl30 lacking the trans-membrane domain -useful as an antagonist for growth factors esp. for ensuring correct development of pre-implantation embryos
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                                                                                                      Gp130; transmembrane domain; growth factor antagonist; embryo pre-implantation; in vitro fertilisation; ss.
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80.0%; Pred. No. 2e+02;
ive 3; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                       Smith SK;
                                                                      Human gp130 splice variant gene.
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Best Local Similarity 80.0
Matches 12; Conservative
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                                                                                                                                                             Homo sapiens.
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   AAT14602;
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Pred. No. 1.9e+02;
3; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The gene encoding human CNTFR was subcloned into bacterial expression vector pcPl10. The resulting plasmid, pRPN151, encoded a recombinant, mature form of human CNTFR. Further manipulation of the coding region optimized expression of the gene in E. coll RFJ26, allowing production of useful amounts
                                                                                                                                                                                                                                                                                               CNTFR; ciliary neurotrophic factor receptor; cytokine; agonist; antagonist; signal transduction pathway; pRPN151; Escherichia coli; ds.
 Indels
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 Mismatches
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(SJUD-) ST JUDE CHILDREN'S RES HOSPITAL.
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                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
289..1407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ihle JN, Stahl N, Yancopoulos GD;
                                                                                                                                                       AAQ83223 standard; cDNA; 1591 BP.
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m
                                                                                                                                                                                                                                                              Human recombinant mature CNTFR
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80.0%;
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289..1404
/*tag= b
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1170 GCTCCAGTCACTCCA 1156
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1170 GCTCCAGTCACTCCA 1156
 Conservative
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                                    1 RCTCCARTCRCTCCA 15
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P-PSDB; AAR70147.
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Best Local Similarity
Matches 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09-SEP-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9507467-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      mat_peptide
12;
                                                                                                                                                                                           AAQ83223;
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Gaps

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RESULT

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AAT14602/ ID AAT14 XX

of

us-09-532-263-7.rng

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immunostimulant; cardiant; thrombolytic; cagaulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antidiabetic; hypotensive; dermatological; immunosuppressive; antidiabetic; hypotensive; dermatological; immunosuppressive; antidinflammatory; antibacterial; antidival; antitinedal; antition; associated disorder. The parbological conditions associated with an ORFX associated disorder. The nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative disorders, osteoarthritis, graft vs host disease, cardiovascular disease, diabetes mellitus, hypothyroidism, cholesterol ester storage, systemic lupus erythematosus, severe combined immunodeficiency (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and cartilage damage, nocturnal haemoglobinuria, antilnfammatory disease; to enhance coagulation; to inhibit thrombosis; and as a contraceptive.
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                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CNTFR; transgenic animal; motorneurone disease; trauma; muscular dystrophy; inflammation; amytrophic lateral sclerosis; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA encoding CNTF receptors - useful in diagnosis, physiological study and treatment of CNTF-related disorders
                                                                                                                                                                                                                                                                                                                                                                                                                    ;
0
                                                                                                                                                                                                                                                                                                                                                                             Score 13.8; DB 21; Length 1419;
Pred. No. 1.9e+02;
3; Mismatches 0; Indels 0;
osteopathic; anticonvulsant; antiarthritic; immunosuppressant;
                                                                                                                                                                                                                                                                                                                          Sequence 1419 BP; 333 A; 436 C; 384 G; 265 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ciliary neurotrophic factor receptor-coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yancopoulos GD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
289..1407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAQ20195 standard; cDNA; 1591 BP.
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/product= CNTFR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 2; Fig 2; 92pp; English
                                                                                                                                                                                                                                                                                                                                                                              92.0%;
80.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  91US-0700677.
90US-0532285.
91US-0676647.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91WO-US03896
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                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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545 gctccagtcactcca 559
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                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
'-haq 12; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1992-007490/01.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-MAY-1991;
01-JUN-1990;
28-MAR-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                03-JUN-1991;
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CNTF has been cloned and syntheisized in eukaryotic as well as bacterial expression systems, as described in International Application No. PCT/U.S. 90/05241. The CNTF receptor (CNTFR or CNTFR or alpha) has been cloned and expressed in eukaryotic cells, as described in U.S. Patent Application Serial No. 07/700,677 and International Application No. PCT/US91/03896, filed June 3, 1991. The present invention relates to a stable CNTF/receptor complex which possesses a different mobility in native polyacrylamide gels than either purified fractions of CNTF or CNTFR.
                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                  Sequence encoding human ciliary neurotrophic factor receptor (CNTF).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cell-free ciliary neurotrophic factor-receptor complex - for diagnosis and treatment of cell proliferation and differentiation disorders e.g. myeloid leukaemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ip N;
Yancopoulos GD;
                                                                                                                                                   ó
and organisms (e.g. E.coli) for the expression of the receptor protein. Monoclonal antibodies can be raised to the CNTF. The can be used as a probe to screen a library for clones encoding members of the family of molecules including IL-6 receptor.
                                                                                                                      Length 1591;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 13.8; DB 14; Length 1591;
Pred. No. 1.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                            Ciliary neurotrophic factor; receptor; protein complex; ds
                                                                                                                                                    Indels
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                                                                        Sequence 1591 BP; 289 A; 545 C; 465 G; 292 T; 0 other;
                                                                                                                      Score 13.8; DB 13;
Pred. No. 1.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Davis S, Everdeen D, Squinto SP, Stahl N,
                                                                                                                                                   3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers 289..1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Fig 2; 122pp; English.
                                                                                                                                                                                                                                                                         AAQ39626/c
ID AAQ39626 standard; cDNA; 1591 BP.
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80.0%;
                                                                                                                      92.0%;
80.0%;
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92US-0865878.
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1170 GCTCCAGTCACTCCA 1156
                                                                                                                   Query Match 92.0
Best Local Similarity 80.0
Matches 12; Conservative
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                                                                                                                                                                                 1 RCTCCARTCRCTCCA
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                     AAQ39626;
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agents capable of modulating the activity of IL-13 and related cytokines such as interleukin-4 for the treatment of allergy, asthma and other conditions relating to IgE. The genetic sequences can
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200058473-A2.
                                       including NR4.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
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                               also
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                     Gaps
                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA encoding animal haemopoletin receptor which interacts with interleukin-13 - useful to treat asthma, allergy or condition
 Length 1193;
                                                                                                                                                                                           NR4; haemoprotein receptor; interleukin-13 receptor; IL-13; cytokine; allergy; asthma; therapy; ss.
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                   Indels
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1/tag= d
//note= "bases 121.123 (nnn) code for
Score 13.8; DB 15;
Pred. No. 1.9e+02;
                                                                                                                                                                        Mouse interleukin-12 receptor alpha chain NR4 DNA.
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                                                                                                                                                                                                                                                                                                                                               unidentified amino acid"
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                   3; Mismatches
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61.1341
/*tag= a
61.141
/*tag= b
142.1338
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nicola NA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (AMRA-) AMRAD OPERATIONS PTY LTD.
                                                                                                             BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            interleukin-13 – useful to tre
exacerbated by IgE production
92.0%;
80.0%;
                                                                                                             AAT66164 standard; DNA; 1383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96AU-0002208.
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                                                                                                                                                   15-JUL-1997 (first entry)
                     12; Conservative
                                                  640..642
                                       1 RCTCCARTCRCTCCA 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1997-259018/23.
          Similarity
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                                                                                                                                                                                                                                                                                                                                                         misc_difference
                                                                                                                                                                                                                                                                                                                  misc_difference
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                                                                                                                                                                                                                                                                           sig_peptide
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                                                                                                                                 AAT66164;
 Query Match
           Best Local
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                   Matches
                                                                                                   AAT66164/c
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Human; open reading frame; ORFX; detection; cytostatic; hepatotropic; vulnerary; antiporiatic; antiparkinsonian; nootropic; neuroprotective; anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant; immunostimulant; thrombolytic; coaquiant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antiinflammatory; antianaemic; gene therapy; cancer; proliferative antithyroid; antianaemic; gene therapy; cancer; proliferative disorder; hypertension; neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; holesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; bone damage; cartilage damage; antiinflammatory disease; coagulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAC7446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames i to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective;
                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                          Length 1383;
be used in prodn. of recombinant NR4 or fusion proteins
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                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                       Sequence 1383 BP; 416 A; 296 C; 315 G; 350 T; 6 other;
                                                                                                                                                                                                                                          92.0%; Score 13.8; DB 18;
80.0%; Pred. No. 1.9e+02;
ive 3; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAC76452 standard; cDNA; 1419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              thrombosis; contraceptive; ss
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02-APR-1999; 99US-0127636.
05-APR-1999; 99US-0127728.
30-MAR-2000; 2000US-0540763.
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Best Local Similarity 80.0
Matches 12; Conservative
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WPI; 1994-263772/32.
                                                                                                                                           Best Local Similarity
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                                                                                                                                                                                                                                                                                      27-MAR-1995
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                                                                                                                                  Query Match
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                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA encoding cytokine-receptor-complementary region G-CSF receptor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 G-CSF; granulocyte colony stimulating factor; receptor; leukaemia; over-proliferation; recombinant; vector; ds.
                                                                    Auto-antigen from synovial cells of rheumatoid arthritis patients binds to antibodies present in these patients, for diagnosis and prediction of the disease
                                                                                                                                        auto-antigen clone A, which can be used to diagnose and predict the development of RA by reaction with antibodies in biological specimens, e.g. sera, from patients.

RNA was isolated from synovial cells from a RA patient and used the construct a cDNA library. This was screened using IgG separated from the synovial fluid of a RA patient. Active clones were isolated in a cloning vector, and inserted into an expression vector for the transformation of E. coli NN522, Transformants on culture express clone A peptide and follistatin related protein
                                                                                                                                                                                                                                                                                                          ;
0
                                                                                                                                                                                                                                                                                     Length 990;
                                                                                                                               The present sequence encodes the rheumatoid arthritis (RA)
                                                                                                                                                                                                                                                                                                           Indels
                     Tanaka M;
                                                                                                                                                                                                                                                        Sequence 990 BP; 321 A; 190 C; 193 G; 286 T; 0 other;
                                                                                                                                                                                                                                                                                    Score 13.8; DB 18;
Pred. No. 1.9e+02;
3; Mismatches 0;
                    Osaki S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /*tag= a
/note= "no stop codon"
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1..999
/*tag= a
                   Osakada F,
                                                                                                           Claim 9; Page 38; 61pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                  BP.
                                                                                                                                                                                                                                                                                     92.0%;
80.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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Best Local Similarity 80.0
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                       into the culture medium.
                                                                                                                                                                                                                                                                                                                             1 RCTCCARTCRCTCCA 15
                    Nakao K,
                                     WPI; 1997-281030/25.
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(KANF ) KANEKA CORP
                                                P-PSDB; AAW17859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P-PSDB; AAR99141
                    Kishimura M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JP08140678-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-NOV-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                         30-0CT-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                     AAT35138;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Key
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AAT35138 encodes a human protein of a ligand binding region of a G-CSF (granulocyte colony stimulating factor) receptor. The DNA and protein are used in the development and/or study of drugs which can be substituted for G-CSF. Such drugs are useful in the traatment of leukaemia resulting from granulocyte over-proliferation. The DNA may be expressed recombinantly to provide a high yield of the protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Survival and/or proliferation of corticospinal neurons or neurons in the subependymal zone in a patient are promoted by administration of recombinant ciliary neurtrophic factor. The protein may be used to treat a wide range of neurological diseases, e.g haemorrhage, tumor, trauma, infection, Alzheimer's disease, Creuzfeld Jokob disease, Down's syndrome, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ciliary neutrophic factor; neurological disease; haemorrhage; tumor; trauma; infection; Alzheimer's disease; Creuzfeld Jakob disease; Down's syndrome; central nervous system; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Promoting survival and proliferation of neurons to - with recombinant human ciliary neurotrophic factor, also new rat receptor for this factor, useful to treat neurological disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                          92.0%; Score 13.8; DB 17; Length 999; 80.0%; Pred. No. 1.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wiegand S, Yancopoulos GD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
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                                                                                                                                                                                                                                                                                                                                       Sequence 999 BP; 207 A; 347 C; 276 G; 169 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rat ciliary neutrophic factor-alpha DNA.
Claim 4; Page 12-14; 17pp; Japanese.
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81..1058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAQ67887 standard; DNA; 1193 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 5; Fig.1; 49pp; English
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AAZ43552 RESULT

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This sequence represents the C-terminal domain of a ligand binding region of a human granulocyte colony stimulating factor (G-CSF) receptor. This sequence, the corresponding mouse sequence (see AAT33515), or a conserved fragment of both these sequences (see AAT33517) can be used in an expression vector for the production of the receptor. The sequences can also be used in an expression vector containing E.coli maltose binding protein to produce a fusion protein. The DNA can be used in the study of diseases related to the interaction between the G-CSF receptor and its ligand, as well as for the treatment or prevention of G-CSF receptor. G-CSF-dependent diseases and abnormalities. The recombinant ligand-binding region produced, is physiologically active and can be used in the study of the G-CSF receptor, such as analysis of its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   92.0%; Score 13.8; DB 17; Length 639; 80.0%; Pred. No. 1.8e+02; 1.ve 3; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                              DNA coding for a ligand-binding region BC of G-CSF receptor useful for prevention or treatment of G-CSF diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rheumatoid arthritis; auto-antigen; clone A; diagnosis; prediction; synovial cell; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 639 BP; 135 A; 227 C; 174 G; 103 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cDNA for rheumatoid arthritis auto-antigen clone A.
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                                                                                                                                                                                                                                           (TANP-) TANPAKU KOGAKU KENKYUSHO KK.
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1..990
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                                                                                                                                         94JP-0278841
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Matches 12; Conservative
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                                                                                                                                                                                                                                                                                                                    P-PSDB; AAW00648.
Homo sapiens.
                                               JP08131172-A.
                                                                                                                                                                                            14-NOV-1994;
                                                                                                                                              14-NOV-1994;
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                                                                                            28-MAY-1996.
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AAT68830/c
δy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This invention describes a novel method (A) of inducing differentiation of a bone marrow stromal progenitor cell to an osteoblastic lineage is new and comprises contacting the bone marrow stromal progenitor cell with an amount of leptin or its analog. The products of the invention have osteopathic activity. The method is useful for inducing differentiation of a bone marrow stromal progenitor cell to an osteoblastic lineage and for inducing bone formation in mammals. Therefore the method is useful for the treatment of osteoporosis and other conditions where bone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      formation is required. This sequence represents a PCR primer used in the amplification of human OB-R variants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Granulocyte colony stimulating factor; G-CSF; C-terminus; mouse; human; ligand binding domain; E.coli; maltose binding protein; receptor; G-CSF-dependent disease; G-CSF abnormality; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Inducing differentiation of bone marrow stromal progenitor cells to an osteoblastic lineage \,\cdot\,
                                                                                                                                                                                                                                                               OB-R; leptin; PCR primer; differentiation; bone marrow; osteopathic; stromal progenitor; osteoblastic lineage; treatment; osteoporosis; ss.
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                                                                   BP.
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                                                                   AAZ43552 standard; DNA; 22
                                                                                                                                                             21-FEB-2000 (first entry)
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Matches 12; Conservative
                                                                                                                                                                                                                Human OB-R PCR primer 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (MAYO-) MAYO FOUNDATION.
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                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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                                                                                                                                                                                                                                                                                                                                   Synthetic
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Query Match

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Gaps

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AAV27138
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                                          5 Degenerate hybridisation probes (AAT17870-74) are based on a conserved motif (AAR92812) found in haemopoietin receptors. The probes are used in the identification and/or cloning of genes coding for novel haemopoietin receptors, e.g. the murine interleukin-11 (IL-11) receptor alpha chain gene (AAT17868). Such receptors are defined by their ability to hybridise to the probes under medium stringency conditions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oligonucleotide HYB2 hybridises under medium stringent conditions to a novel DNA (see AAT64442) encoding human haemopoietin receptor NR2 (AAW14841). It was used in the isolation of a partial NR2 sequence from a CDNA library constructed from the bone marrow mRNA of a patient recovering from chemotherapy. NR2 and genetic sequences encoding it can be used in the development of (ant)agonists, therapeutics and diagnostic reagents based on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human haemopoietin receptor NR2, and corresponding DNA - used e.g.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Haemopoietin receptor; new receptor 2; NR2; leptin; human; autoimmune disease; nervous system; cerebral palsy; trauma induced paralysis; vascular ischaemia; stroke; neuronal tumour; motor neurone disease; Parkinson's disease; Huntington's disease; Alzheimer's disease; multiple sclerosis; peripheral neuropathy; heavy metal; alcohol; toxicity; kidney! failure; infectious disease; herpes; rubella; measles; chicken pox; HIV; HTLV-1; therapy; probe; ss.
                                                                                                                                                                                                                                                                                                               Length 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Haemopoietin receptor NR2 hybridising oligonucleotide HYB2
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100.0%; Pred. No. 1.4e+02;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                         Sequence 15 BP; 2 A; 7 C; 0 G; 3 T; 3 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   for treatment of autoimmune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ligand interaction with the receptor
Claim 12; Page 51; 87pp; English.
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                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 15; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Haemopoietin receptor; cell proliferation; cell differentiation; cancer; cell survival; therapeutic; neuronal proliferation; drug screening; ss;
                                                                     Gaps
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eda M, Nash A, Nicola NA, Rakar S, Willson T;
                   Length 15;
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                 Score 13.8; DB 18;
Pred. No. 1.4e+02;
0; Mismatches 0;
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iive 0; Mismatches 0;
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92.0%; Scc.
100.0%; Pre
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(DZIE/) DZIEGLEWSKA H E.
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-- T, Maeda M,
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                 Query Match
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Zhang J;
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Thu Aug 30 10:41:31 2001

gp130 N-terminal f Human haemopoietin Murine leptin rece Murine leukaemia i

Human recombinant Human gp130 splice fortuitum plasm Human haemopoletin

AAV69318 AAC92350

AAQ83223 AAT14602

AAQ74081 AAC92338 AAQ5541 AAQ55801 AAQ5802 AAQ92271 AAT98534 AAQ13853 AAQ135703 AAQ135703

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Mouse interleukin-
Human ORFX ORF2007
Ciliary neurotroph
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Human G-CSF recept
CDNA for rheumatoi
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Haemopoietin recep
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31.258 Million cell updates/sec
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                                                                                                                                    August 29, 2001, 20:16:40; Search time 301.32 Seconds
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**SiDSB / goddata/geneseq_/geneseq_NAl1980 . DAT :*

**SiDSB / goddata/geneseq_/geneseq_NAl1981 . DAT :*

**SiDSB / 
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                    GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                       730101 seqs, 313950809 residues
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Maximum Match 100%
Listing first 45 summaries
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AAZ43552
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AAT66164
AAC76452
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Gapop 10.0 , Gapext 1.0
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Murine leukaemia i	R. Mus musc	Mouse LIF'R CLone Murine leukaemia i	Natural splice var	Human GCSF recepto	Murine Leptin rece Encodes granulocyt		G-CSFR cDNA clone	Coding sequence fo	Ob protein recepto	Murine leptin rece	Human gpl30 native	Murine WSX recepto	Haematopoietin rec	numan OB-R Vallanic	Human OB-R variant	Variant form of hu	Clone 25-1 encodes	Human granulocyte	Human GCSF recepto	Human granulocyte Coding sequence fo	SJ									Ω.													contain	hain - used	
AAQ55941	AAQ25800	AAU58426 AA092271	AAT98534	AAQ13857	AAT / 5 / 03 AAO 11579	AAT47099	AAQ95481	AAT98532	AA19/149	AAT75706	AAT14603	AAT85578	AAT12913	AA193/01	AAT95780	AAT74022	AA011580	AAT47100	AAQ13856	AAA62841 AAT98533	ALIGNMENT			ď.				HYB2.		; IL-11; rec	nybriaisation;								LTD.				haemopoietin recep	IL-11 receptor alpha c	t.s
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ALO24826.

ALO24826.

ALO24826.

GSS; genome survey sequence.

Takifugu rubripes.

Takifugu rubripes.

Takifugu rubripes.

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;

Actinopterygii; Neopterygii; Teleostei; Neoteleostei;

Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;

Tetraodontidae; Takifugu.

SE Igar, G., Clark, M., Smith, S., Meek, S., Warner, S., Umrania, Y.,

Williams, G. and Brenner, S.

Direct Submission

Submitted (09-JUN-1998) MRC Human Genome Mapping Project Resource Centre, Hinxton, Cambridge, CBIO 15B, UK. Email:

Vector: pBluescript II KS

VLYpe: phagemid

PRIMER: KS
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Fugu rubripes GSS sequence, clone 006118bD2, genomic survey
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Pred. No. 2.4e+03;
3; Mismatches 0; Indels 0;
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Pred. No. 2.4e+03;
3; Mismatches 0; Indels 0;
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/creamism="Takifugu rubripes"
/db_xref="taxon:31033"
/clone_11b="cosmid 006118"
/clone="006118bp2"
a 85 c 91 g 92 t
/sex="hermaphrodite, male"
/tissue_type="whole animal"
/dev_stage="varied"
69 c 74 g 86 t
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80.0%;
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Matches 12; Conservative
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Best Local Similarity 80.0
Matches 12; Conservative
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AUTHORS
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JOURNAL
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Search completed: August 29, 2001, 19:22:13 Job time: 24136 sec

ORGANISM

REFERENCE

AUTHORS

TITLE JOURNAL

COMMENT

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Caenorhabditis elegans.

Caenorhabditis elegans

Caenorhabditis elegans

Eukaryota: Metazoa, Nematoda; Chromadorea; Rhabditida; Rhabditoidea

1 (bases 1 to 360)

Kohara,Y., Motohashi,T., Tabara,H., Watanabe,H., Sugimoto,A., Sano

M., Miyata,A. and Nishigaki,A.

Expression map of the C.elegans genome

Unpublished (1996)
                Washington University School of MedicineP
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:454254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C65854 360 bp mRNA bol C65854 Yuji Kohara unpublished cDNA Caenorhabditis elegans cDNA
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Pred. No. 2.4e+03;
3; Mismatches 0; Indels
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Sztain="CB1489 him-8(e1489)"
/db_xref="taxon 6239"
/clone="yk395h5"
                                                                                                                                                                                                                                                 Seq primer: -28ml3 rev2 ET from Amersham High quality sequence stop: 209. Location/Qualifiers
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Tel: 81-559-81-6854
Fax: 81-559-81-6855
                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="Soares mouse NML"
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Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                 /organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE:737206"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Yuji Kohara
Gene Library Lab
National Institute of Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="Liver"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: ykohara@lab.nig.ac.jp.
Location/Qualifiers
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80.0%;
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Best Local Similarity 80.0
Matches 12; Conservative
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104 GCTCCAGTCACTCCA 90
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COMMENT
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C65854
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/strain="016 Gujarar"
/strain="016 Gujarar"
/db_xref="taxon:6238"
/clone_lib="kwabara Mixed stage C. briggsae"
/clone_lib="kwabara Mixed stage C. briggsae"
/note="Vector: Lambda gil0; Site_l: EcoRI; Site_2: EcoRI;
Stage:mixed, Sex:hermaphrodite. Library construction:
First strand oligo(dT) primed. Second strand was as per
Gubler/Hoffman. Ligated to EcoRI adaptors. Library is
non-directional. Library is non-normalized. Library
constructed by P.E. Kuwabara. Additional details on
constructed by P.E. Kuwabara are described in P.E.
Kuwabara and S. Shah, NAR 22: 4414 - 4418 (1994). Adaptor
sequence: GAATTC CGTTGCTGCTG"

94 a 52 c 119 g 84 t 3 others
                Eukaryotta; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.

1 (bases 1 to 35.2)

1 (bases 1 to 16.2)

1 Halllacr, L., Chiapelli, B., Chissoe, S., Clark, N., Couch, J., Dubuque, T., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Kuwabara, P., Le, M., Mardis, E., Martra, M., Parsons, J., Rifkin, L., Rohlfing, T., Tan, F., Trevaskis, E., Wateston, R., Wohldmann, P. and Wilson, R., Washington University Caenorhabditis briggsae EST project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        va75c12.r1 Soares mouse NML Mus musculus cDNA clone IMAGE:737206 5/
similar to gb:D17444 Mouse mRNA for soluble D-factor/LIF receptor,
complete (MOUSE);, mRNA sequence.
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Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                          PCR_E: TGTAAAACGACGCCAGTGAGCAAGTTCAGCCTGG
PCR_B: CAGCAAACAGCTATGACTATGAGTATTCTTCCAGGGTA
Source: Washington University Genome Sequencing Center
PCR amplified DNA is available from Washington University Genome
Sequencing Center. Aliquots of the library may be requested from P.
Kuwabara (Pek@mrc-imb.cam.ac.uk).
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seq primer: Commercially available M13 reverse dye primer.
Location/Qualifiers
                                                                                                                                                                                                                              Unpublished (1995)
Contact: Marra MA
Washington University Genome Sequencing Center
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 13.8; DB 187; Length 352;
Pred. No. 2.4e+03;
3; Mismatches 0; Indels 0;

    352
    /organism="Caenorhabditis briggsae"

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The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                          Email: mmarra@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA272591.1 GI:1910922
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80.0%;
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                                                                                                                                                                                                                                                                                                                                                                 Tel: 314 286 1455
Fax: 314 286 1810
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BASE COUNT ORIGIN

Matches

õ g AA272591/C LOCUS DEFINITION

RESULT

ACCESSION VERSION KEYWORDS SOURCE

ORGANISM

REFERENCE AUTHORS TITLE JOURNAL

source

FEATURES

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Gaps

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Senome Exploration Research Group, Life Science Tsukuba Center,
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                                                                       Sciences Center
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                                                                                                                                                                                                                                                        Fax: +55-11-2707001

Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?ti=&t2=QV1-BT0631-280
200-084-f01_1&t3=2000-02-28&t4=1)
200-084-f01_1&t3=2000-02-28&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 321.

Location/Qualifiers
1. .31

Location/Qualifiers
1. .31

Ab_xref="taxon:9606"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/dev_stage="Adult"
/dev_stage="Adult"
/dev_stage="Adult"
/noce="Organ: breast; Vector: puc18; Site_1: Sma1; Site_2: Sm21; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196
/716 - Ludwig Institute for Cancer Research) profiles
into the pUC 18 vector: Reverse transcription of tissue mRNA and cDNA amplification were performed under low
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 31)

S Konno, H., Aizawa, K., Akahira, S., Akiyama, J., Arakawa, T., Carninci, P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Iazawa, M., Radota, K., Kagawa, J., Kai, C., Kawai, J., Kikuchi, N., Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kusakabe, M., Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y., Ono, T., Owa, C., Saito, H., Sakai, C., Sato, K., Shibata, K., Shigemoto, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Shibata, Y., Yano, R., Yano, R., Watahiki, H., Tagawa, A., Takahashi, F., Tominaga, N., Toya, T., Yano, R., Yano, R., Watahiki, A., Watanabe, S., Yamamura, T., Yamanaka, I., Yano, R., Yano, R., Yano, M., Muramatsu, M. and Hayashizaki, Y., Soshida, K., Yoshiki, A., Yoshida, M., Muramatsu, M. and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                          Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                       Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Pred. No. 2.4e+03;
3; Mismatches 0; Indels 0;
                                              Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
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Contact: Yoshihide Hayashizaki
                                                                                                                     Contact: Simpson A.J.G.
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80.0%;
                                                                                                                                                                                                                                           rel: +55-11-2704922
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Best Local Similarity 80.0
Matches 12; Conservative
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Simpson, A.J.
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                                                                                                                                                                                                                    Brazil
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BB209387/c
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                       TITLE
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Email: genome-resettc.riken.go.jp,
UKL: http://genome.rtc.riken.go.jp,
UKL: http://genome.rtc.riken.go.jp,
Carninci,P. Nishiyama.Y., Westover,A., Itch,M., Nagaoka,S., Sasaki,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length CDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itch,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki,Y.
Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
Please visit our web site (http://genome.rtc.riken.go.jp) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pstacl2.rl Kuwabara Mixed stage C. briggsae Caenorhabditis briggsae ConA similar to SP:B0280.5, mRNA sequence.
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                The Institute of Physical and Chemical Research (RIKEN), Genomic
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/db_xref="taxon:10090"
/clone="#430092P05"
/clone="#430092P05"
/clone=lib="RIKEN full-length enriched, 0 day neonate thymus"
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Pred. No. 2.4e+03;
3; Mismatches 0; Indels 0;
                                                  3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: +81-298-36-9013
Fax: +81-298-36-9098
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/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="thymus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
Senome Science Laboratory
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MEDLINE COMMENT

FEATURES

JOURNAL

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/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="b030001N11"
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Best Local Similarity
Matches 12; Conserv
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalla; Eutherla; Rodentla; Sciurognathi; Muridae; Murinae; Mus.

1 (basa, 1 to 295)

Alzawa,K., Akahira,S., Akimura,T., Arai,A., Arakawa,T., Carninci,P., Hanagaki,T., Hayatsu,N., Hiraoka,T., Hirozane,T., Hodoyama,Y., Imotani,K., Ishil,Y., Itoh,M., Izawa,M., Kawai,J., Kojima,Y., Konno,H., Kusababe,M., Matsuyama,T., Miyazaki,A., Nakamura,M., Nishi,K., Numazaki,R., Sato,K., Shibata,K., Sakai,C., Sakai,C., Sakai,C., Sakai,C., Sakai,C., Sato,K., Suzuki,H., Tagawa,A., Takahashi,F., Tanaka,T., Toya,T., Watahiki,A., Yamamura,T., Yasunishi,A., Yoshida,K., Kike Mouse Ests (Alzawa,K. et al. 2000)

L Unpublished (2000)

Contact: Yoshihide Hayashizaki
                                                                                                                                                                    Tal: +55-11-2704922

Fax: +55-11-2707001

Bmail: asimpsoneludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=MRI-Cr0355-160 200-003-f04643=200-002-16644=1)

Seq primer: puc 18 forward: 20
High quality sequence start: 20
High quality sequence stop: 281.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Organ: colon; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ONESTES PCR (U.S. Letters Patent application No. 196 ,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
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                                               Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genome Science Laboratory
The Institute of Physical and Chemical Research (RIKEN), Genomic
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Pred. No. 2.4e+03;
3; Mismatches 0; Indels 0;
Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="CT0355"
/dev_stage="Adult"
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80.0%;
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Best Local Similarity 80.0
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70 ACTCCAGTCACTCCA 56
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BB599621/c

RESULT

ó a ACCESSION VERSION

ORGANISM

REFERENCE AUTHORS

KEYWORDS SOURCE

TITLE JOURNAL COMMENT

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Email: genome-resertc.riken.go.jp,
URL:http://genome.rtc.riken.go.jp,
URL:http://genome.rtc.riken.go.jp/
Carninci,P., Nishiyama.Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki
,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by
trehalose and its application for the synthesis of full length
cDNA. Proc. Natl. Acad Scl. U.S.A. 95 (2), 50.524 (1998)
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
Y. and Hayashizaki,Y., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki
,Automated filtration-based high-throughput plasmid preparation
system. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
I (bases 1 to 321)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., ad Silvay,W. Jr., Zago,M.A., Bordin,S., Coste,F.F., Nagai,M.A., Garcia,Coste,F.F., Bataskima,A., Bataskima,A., Baia,G.S., Simpson,D.H., Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                prepared by using trehalose thermo-activated reverse
transcriptuse and subsequently enriched for full-length by
cap-trapper. Second strand cDNA was prepared with the
primer adapter of sequence [5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Please visit our web site (http://genome.rtc.riken.go.jp) for
further details.
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Pred. No. 2.4e+03;
3; Mismatches 0; Indels 0;
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trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh, M., Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J., Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki, Y., and Hayashizaki, Y.
Automated filtration-based high-throughput plasmid preparation carninci, P. and Hayashizaki, Y.
Carninci, P. and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 281)

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carralho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Thermostabilization and thermoactivation of thermolabile enzymes by
                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="cerebellum"
/dev_stage="7 days neonate"
/lab_host="7 days neonate"
/lab_host="9110"
/lab_host="1 sall; Site_2: BamHI; cDNA library was
/note="51te_1: Sall; Site_2: BamHI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
project of Genome Exploration Research froup in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN. Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
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MR1-CT0355-160200-003-f04 CT0355 Homo sapiens CDNA, mRNA sequence.
AW859532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                       High-efficiency fuil-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
Please visit our web site (http://genome.rtc.riken.go.jp) for further details.
                                                                                                                                                                                                                                                                                            /organism="Mus musculus"
/db_xref="taxon:10090"
/clone="A730085006"
/clone_lib="RIKEN full-length enriched, 7 days neonate
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Pred. No. 2.4e+03;
3; Mismatches 0;
                                                                                                                                                                                                                                                                     Location/Qualifiers
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Best Local Similarity
Matches 12; Conserv
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AW859532/c
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           Email: asimpsonelludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/seq/gethtml.pl?tl=IL&t2=IL-BT161-010.html &t3=080399&t4=1)
Seq primer: puc 18 forward.
Location/Qualifiers
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URL:http://genome_rtc.riken.go.jp,
Carintoi.p., Nishiyama,Y. Westover.A., Itoh,M., Nagaoka,S., Sasaki,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
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The Institute of Physical and Chemical Research (RIKEN), Genomic
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Genome Exploration Research Group, Life Science Tsukuba Center,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 13.8; DB 103; Length 254;
pred. No. 2.4e+03;
3; Mismatches 0; Indels 0;
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Tel: +81-298-36-9013
Fax: +81-298-36-9098
                                                                                                                                                            / Crganism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="B1161"
/sex="female"
/dev_stage="Adult"
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BB258685.1 GI:8951518
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163 ACTCCAGTCACTCCA 177
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'N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by trebalose and its application for the synthesis of full length CDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J., Tomaru,Y., Carnholi,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki,Y. and Hayashizaki,Y. Albata,Y., Ozawa,Y., Muramatsu,M., Okazaki Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
Carnholi,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
Please visit our web site (http://genome.rtc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 242)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
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MR1-CT0355-180200-006-c12 CT0355 Homo sapiens CDNA, mRNA sequence.
AW859572
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Pred. No. 2.4e+03;
3; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Mismatches
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="4930578B11"
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/dev_stage="adult"
/lab_host="DH10B"
                                                                                                                                                                                                                                       further details.
Location/Qualifiers
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80.0%;
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/organism="Homo saplens"
/db_xref="texton:9606"
/db_xref="texton:9606"
/clone_lib="CT0355"
/dev_stage="Adult"
/note="Organ: colon; Vector: pucl8; Site_l: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196; 716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low
                                                                                                                                                                                                                                                            Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl-&t2-MR1-CT0355-180
Seq primer: puc 18 forward
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Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Shotgun sequencing of the human transcriptome with ORF expressed
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IL-BT161-080399-010 BT161 Homo sapiens CDNA, mRNA sequence.
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000) 20202663
                                        U.S.A. 97 (7), 3491-3496 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            High quality sequence start: 9
High quality sequence stop: 242.
Location/Qualifiers
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58 c 40 g
sequence tags
Proc. Natl. Acad. Sci.
                                                                                                        Contact: Simpson A.J.G.
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AI907996.1 GI:6498676
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Unpublished (1999)
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Email: genome-res@rtc.riken.go.jp,
URL:http://genome.rtc.riken.go.jp,
Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.
Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
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                                                                                                                                                                                                                                                                                                                                             /organism="Mus musculus"
//organism="taxon:10090"
//clone="A33006114"
//clone_lib="RIKEN full-length enriched, adult male spinal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note-"Site_1: Sall; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in
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Kim,T.O., Hong,Y.C., Yu,H.S., Hwang,M.Y., Yun,H.C., Kong,H.H. and Chung,D.I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AT002416 199 bp mRNA EST 10-SEP-1999 AT002416 Entamoeba histolytica trophozoite Entamoeba histolytica cDNA clone En044, mRNA sequence.
                                                                                                                                                                                                                                                     19-44 (1999)
Please visit our web site (http://genome.rtc.riken.go.jp) for
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Pred. No. 2.3e+03;
3; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Entamoeba histolytica trophozoite EST
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Entamoeba histolytica
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80.0%;
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51 ACTCCAGTCACTCCA 65
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Best Local Similarity
Matches 12; Conserv
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"S Konno, H., Pukuda, S., Akiyama, J., Arakawa, T., Carninci, P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Horli, F., Ishi, Y., Ishikawa, J., Ishikawa, T., Itoh, M., Izawa, M., Kadota, K., Kagawa, J., Kai, C., Kawai, J., Kikuchi, N., Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kusakabe, M., Matsuyama, T., Miki, F., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y., Oda, C., Saito, H., Sakai, C., Sato, K., Shibata, Y., Shigemoto, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Sugahara, Y., Suzuki, H., Suzuki, H., Tagawa, A., Takahashi, F., Tominaga, N., Toya, T., Tsunoda, Y., Watahiki, A., Watanabe, S., Yamanura, T., Yamanaka, I., Yano, R., Yasunishi, A., Yokota, T., Yoshida, K., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.
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URL:http://genome.rtc.riken.go.jp/
Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:5759"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BB018457 23-JUN-2000
BB018457 RIKEN full-length enriched, adult male testis (DH10B) Mus
musculus cDNA clone 4930578B11 3', mRNA sequence.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 232)
                                                                                                                                                                                            Email: dichungebh.kyungpook.ac.kr
Submitted through BRIC(Biological Research Information Center) of
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Genome Exploration Research Group, Life Science Tsukuba Center,
Genome Science Laboratory
                                                             Kyungpook National University School of Medicine
Dong-in dong 101, Chung-gu, Taegu 700 - 422, Republic of Korea
Tel: 82-53-420-6958
Fax: 82-53-422-9330
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Pred. No. 2.4e+03;
3; Mismatches 0; Indels
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Tel: +81-298-36-9013
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Contact: Chung DI
Department of Parasitology
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BB018457.1 GI:8190064
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80.0%;
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Best Local Similarity 80.0
Matches 12; Conservative
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Eco RI s Tissue	CDNA Li CDNA Li	Clone d found th		FEATURES									BASE COUNT ORIGIN		Query Match	Matches 12; Con	Qy 1 RCTCCARTCR	102	1	RESULT 2	BB189498 LOCUS BB189498	DEFINITION BB189	ACCESSION BB189498	SO	SOURCE house mo ORGANISM Mus musc	Eukaryot Mammalia	REFERENCE 1 (base AUTHORS Konno, H.	,P., End Hirozane Trawa M	Kiyosawa , Matsuy	, Ono,Τ., Y., Shi	, Suzuki ,T., Tsu		JOURNAL Unpublis COMMENT Contact:	Genome S	The inst Sciences 3-1-1 Ko
	Description	AW408083 UI-HF-BM0 BB189498 BB189498	BB018457	ANG 393/2 MKI -CIO33 AI907996 IL-BI161-	BB258685 BB258685 AW859532 MR1-CT035	BB599621 BB599621	BE080913 QV1-BT063 BB209387 BB209387	R04486 pk24c12.rl AA272591 va75c12.r	C65854 C65854 Yuji	AL024820 FUGU FUDE AV401050 AV401050	AV698306 AV698306 AA984710 am90a11 s	AW489097 UI-M-BH3-	AA663262 ab80f07.s	AQ060441 CIT-HSP-2 AV523125 AV523125	AV743168 AV743168 N75185 VW33300 T1	BF70509 7 2000 11	BGZ63/54 WHE2348_F AQ663435 HS_2160_B	AQ332979 HS_5005_B AQ667104 HS_2106_B	AA619632 v154409.r	AA495324 fa01c03.r	R/3050 yj94112.rl AW279627 fj42c06.x	T21895 3903 Lambda A2151949 SP 0006 B	BF820788 MT1-RT004	AQ648347 RPC193-EC	ס	AT005091 AT005091 BF200134 WHE2252 D	AQ668275 HS_2121_B			EST 16-FEB-2000	-UI.rl NIH_MGC_38 Homo sapiens cDNA clone NA sequence.		. Vertehrata. Futeleostomi.	ni; Hominidae; Homo.	1 (USSES 1 to 140) NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC)
SUMMARIES	ID	.5 AW408083 7 BB189498	BB018457	AI907996	BB258685 AW859532	BB599621	BE209387 ·	R04486 A272591	C65854	AV401050	AV698306 AA984710	AW4 89097	AA663262	AQ060441 AV523125	AV743168 N75185	BF706981	BG263754 AQ663435	AQ332979 AQ667104	A619632	A495324	R/3050 AW279627	T21895 A2151949	BF820788	AQ648347	AI311382 9 BF776672	AT005091 BF200134	AQ668275	ALIGNMENTS		mRNA	UI-HF-BMO-adu-d-10-0-UI.rl NIH_MGC_38 IMAGE:3062850 5', mRNA sequence.		Ordata. Granjatz	imates; Catarrh	.nih.gov/. Health, Mammal
	- 1	127	123	103	129	161	128	187 4 A	156	30	32	116	10	223 31	110	168	231	227	6	1 60	114	239	170	231	18 169	106 145	231			140 bp	0-0-U mrna	27140	٠.	a; Pr	<pre>1 (bases 1 to 140) NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, M</pre>
	Query Match Length DB	140	232	254	279	295	321 331	352 355	360	364	368 381	387	408	408	423	424	4 26 4 28	435	444	44	455 455	455	4 5 4 5 8 8 8	462	463	471	482			140	adu-d-1 850 S',	GI:6927140	ins Metazo	Eutheri	tp://mg .tp://mg .nstitut
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Ino, H. Aizawa, K., Akahira, S., Akiyama, J., Arakawa, T., Carninci, A., Endo, T., Fukuda, S., Rkuishi, Y., Hara, A., Hayatsu, N., Cozane, T., Hori, F., Ishii, Y., Ishikawa, J., Ishikawa, T., Itoh, M., Yawa, M., Kadotca, K., Kogawa, I., Kal, C., Kawai, J., Kkuchi, N., Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y., Nosawa, H., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y., Noo, T., Owa, C., Saito, H., Sakai, C., Saco, K., Shibata, Shigemcto, Y., Shinaqawa, A., Takahashi, F., Tominaga, N., Toya, Tsunoda, Y., Watahiki, A., Yokota, T., Yoshida, K., Yoshiki, A., Yokota, T., Yoshida, K., Yoshiki, A., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.
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cgapbs-r@mail.nih.gov
    site shown at the beginning of the sequence.
    Procurement: Louis M. Staudt, M.D., Ph.D.
    Library Preparation: M.B. Soares Lab
    Library Arrayed by: M.B. Soares Lab
    equencing by: M.B. Soares Lab
    cistribution: MGC clone distribution information can be
    through the I.M.A.G.E. Consortium/LLNL at:
    o.llnl.gov/bbp/image/image.html
    imer: M13 Forward.
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Exploration Research Group, Life Science Tsukuba Center,
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Pred. No. 2.3e+03;
3; Mismatches 0; Indels 0;
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11-298-36-9013
11-298-36-9098
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98 GI: GI:8850069
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9b_est110:*
9b_bt:*
em_gss_hum:*
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em_gss_hum:*
em_gss_hum;*
em_gss_hum;

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

9b_9ss30:*
9b_9ss31:*
9b_9ss31:*
9b_9ss33:*
em_9ss_inv4:
em_9ss_rod6:
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; Search time 3770.35 Seconds (without alignments) 37.607 Million cell updates/sec
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     GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                             OM nucleic - nucleic search, using sw model
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Maximum DB seq length: 2000000000
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gb_est39:*
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                                                                                           Scoring table:
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                                                                                                            Searched:
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em_estpl4:*
em_estpl5:*
em_estpl7:*
em_estpl7:*
em_estpl9:*
em_estpl9:*

em_estro2: em_estro3: em_estro4: em_estro5: em_estro6: em_estro7:

em_estro1

em_estin2:*
em_estin3:*
em_estin4:*
em_eston1:*
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em_estpl2:*
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em_estro19:* em_estro20:* gb_est25:*

gb_est26::
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gb_est30::
gb_est31::
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9b_est41: 9b_est42: 9b_est43: 9b_est44: 9b_est45: 9b_est46:

em_estro8:*
em_estro10:*
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em_estro17:*

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Thu Aug

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ENRAGVGGTVCICHMLTREPSQTSIYQLDLWAGKQLLWNSSEKPSEHVKPPAPRNLTV
HADISHTWLLTWNNPYPSDNLLYSELTYLVNISNENDPTDFRTYNVTYMGPTLRVAAS
TLRSGASYSARVKAWAQSYNSSWSAWSPSTKWLNYYEDTWEQRLQLGVGISCVIVLAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product-"interleukin-4 receptor alpha chain"
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/db_xref="G1-22317"
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                  AF081273 704 bp mRNA MAM 03-MAR-1999 Bos taurus interleukin-4 receptor alpha chain mRNA, partial cds. AF081273 GI:4322316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 704)
Trigona, W.T. and Estes, D.M.
Cloning of bovine homolog to interleukin-4 receptor alpha chain Unpublished
2 (bases 1 to 704)
Trigona, W.T. and Estes, D.M.
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Submitted (29-JUL-1998) Veterinary Pathobiology, University of
Missouri-Columbia, 201 Connaway Hall, Columbia, MO 65211, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Bos taurus"
/db.xref="taxon:9913"
/cell_type="peripheral blood activated T lymphocytes"
<1. >704
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Pred. No. 2.1e+03;
2; Mismatches 1;
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Best Local Similarity 80.0
Matches 12; Conservative
                              1 RCTCCANGCRCTCCA 15 :||||| ||:|||||| 309 GCTCCAGGCACTCCA 295
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561 GCTCCACGCGCTCCA 547
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2006 c 206 g 138 t
                                                                                                                                                                                                                            /translation="MKLLSSIEQACDICRLKKLKCSKEKPKCAKCLKNNWECRYSPKT
KRSPLTRAHZEVERELEKDLFLFLPENDLDHILKMDSLODIRALLGGLFVODNV
KRDAYTDRLASVETDAKLTLKQHRISATSSEESSNKGORG/IVSTAPPTDVSLGDEL
HLDGEDVAMAHADALDDFDLDMLGDGDSPGFGFTPHDSAPYGALDMADFEFEQMFTDA
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 701)
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Submitted (16-FEB-2000) Graw J., Institute of Mammalian (GSF-National Research Center for Environment and Health, Ingolstædter Landstr. 1, D-86764 Neuherberg, GERMANY Location/Qualifiers
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Mus musculus mRNA for beta-A2-crystallin (cryba2 gene).
AJ272227
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/function="lens structural protein"
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Pred. No. 2.1e+03;
2; Mismatches 1;
                                                                                                               /note="unnamed protein product"
/codon_start=1
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                                                                                                                                                                     /protein_id="CAA03823.1"
/db_xref="GI:4530778"
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/db_xref="taxon:10090"
1. .701
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beta-A2-crystallin; CRYBA2 gene.
                                                      db_xref="taxon:32644"
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/gene="cryba2"
64. .657
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Best Local Similarity 80.0%;
Matches 12; Conservative
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Best Local Similarity 80.0
Matches 12; Conservative
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/gene="CRYBA2"
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           88.0%;
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           Query Match 88.0
Best Local Similarity 80.0
Matches 12; Conservative
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275 ACTCCAGGCGCTCCA 261
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291 GCTCCAGGCACTCCA 277
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                                                                                                                                                                                                                                                                                                     /product="prolactin receptor"
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/db_xref="G1:999115"
/db_xref="G1:9
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/gene="beta-A2"
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1 (bases 1 to 696)

van Rens,G.L.M., Driessen,H.P.C., Nalini,V., Slingsby,C., de Jong,W.W. and Bloemendal,H.
Isolation and characterization of CDNAs encoding beta-A4-crystallins: Heterologous interactions in the predicted dene 102, 179-188 (1991)
entry [NCBI glbbsq 168377] from the original journal article.
This sequence comes from Fig. 5.
Location/Qualifiers
1. offon/Outlifiers
//organism="Homo sapiens"
//db_xref="taxon:9606"
//cell_line="Br474"
//cell_type="breast cancer"
/1. 621
//note="This sequence comes from Fig. 5; hPRL receptor"
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Cow beta-A2 crystallin (beta-A2) mRNA, complete cds.
M60329
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Bos taurus cDNA to mRNA.
Bos taurus
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/organism="Bos taurus"
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46. .639
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80.0%;
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585 ACTCCATGCACTCCA 571
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30...623
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/gene="CRYBA2"
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YQYVLERDRHSGEFCTYGELGTQAHTGQLQSTRRVQH"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (abses 1 to 700)
Wistow, G.
Direct Submission
                                               Gaps
                                                                                                                                                                                                                         AF166331 700 bp mRNA PRI 22-JUL-1999
Homo sapiens beta crystallin A2 (CRYBA2) mRNA, complete cds.
AF166331
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Haseloff,Jr. and Hodge,S.
Hareloff,Jr. and Hodge,S.
Patent: WO 9730164-A 1 21-AUG-1997;
MEDICAL RES COUNTL (GB)
Other publication AU 1801497 19970902.
Location/Qualifiers
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Pred. No. 2.1e+03;
Score 13.2; DB 7;
Pred. No. 2.1e+03;
2; Mismatches 1;
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/db_xref="taxon:9606"
1. .700
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Sequence 1 from Patent WO9730164.
A64741
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Web : www.genoscope.cons.fr)
The CDNA library to be analyzed within the framework of this project was created using a Botrytis cinerea strain which was grown under conditions of nitrogen deprivation, which is the normal situation for B. cinerea during its development on its host plant. The library was produced in an oriented direction, in the pBSII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (01-SEP-1999) Genoscope - Centre National de Sequencage :
CP 5706 91057 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (01-SEP-1999) Phytopathologie, INRA, route de St Cyr, 78026 Versailles, France
2 (bases 1 to 607)
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                                                                                                                                                                          Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation.
      Gaps
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                                                                                                                                                                                                                                                                                                                                        Eukaryota; Fungl; Ascomycota; Pezizomycotina; Leotiomycetes; Helotiales; Sclerotiniaceae; Botryotinia.

1 (bases I to 607)

Bitton, F., Levis, C., Fortini, D., Pradier, J.M. and Brygoo, Y. Direct Submission
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Fuh, G. and Wells, J.A.
Prolactin receptor antagonists that inhibit the growth of Gancer cell lines
J. Biol. Chem. 270 (22), 13133-13137 (1995)
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Pred. No. 2.1e+03;
2; Mismatches 1; Indels 0
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Homo sapiens prolactin receptor mRNA, partial cds.
S78505
S78505.1 GI:999114
    Indels
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132 c 145 g 157 t 1 othe
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      1;
      Mismatches
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Botryotinia fuckeliana.
Botryotinia fuckeliana
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80.0%;
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Best Local Similarity 80.0
Matches 12; Conservative
    12; Conservative
                                           1 RCTCCANGCRCTCCA 15
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                                                            Homo sapiens
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                                                      Direct Submission
Submitted (01-SEP-1999) Genoscope - Centre National de Sequencage :
CP 5706 91057 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
Web : www.genoscope.cns.fr)
The cDNA library to be analyzed within the framework of this
project was created using a Botrytis cinerea strain which was grown under conditions of nitrogen deprivation, which is the normal situation for B. cinerea during its development on its host plant:
The library was produced in an oriented direction, in the pBSII
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Submitted (01-SEP-1999) Phytopathologie, INRA, route de St Cyr, 78026 Versailles, France
2 (bases 1 to 600)
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Helotiales; Sclerotiniaceae; Botryotinia.
1 (bases 1 to 600)
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BOLTYLIS cinerea strain T4 cDNA library under conditions of AL112779
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132 c 143 g 158 t
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/organism="Botryotinia fuckeliana"
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Pred. No. 2.1e+03;
2; Mismatches 1;
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131 c 142 g 158
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CDNA library: nitrogen deprivation.
Botryotinia fuckeliana.
Botryotinia fuckeliana
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/db_xref="taxon:40559"
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16 ACTCCAAGCACTCCA 30
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Direct Submission
Submitted (01-SEP-1999) Genoscope - Centre National de Sequencage : Stanfited (01-SEPR cedex - FRANCE (E-mail : segref@genoscope.cns.fr
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(Dases 1 to 540)
Bitton,F., Levis,C., Fortini,D., Pradier,J.M. and Brygoo,Y.
Direct Submission
Submitted (01-SEP-1999) Phytopathologie, INRA, route de St Cyr, 78026 Versailles, France
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(dases 1 to 600)

Bitton,F., Levis,C., Fortini,D., Pradler,J.M. and Brygoo,Y.
Direct Submission
Submitted (01-SEP-1999) Phytopathologie, INRA, route de St Cyr,
                                           Gaps
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BOLTYLIS cinerea strain T4 cDNA library under conditions of nitrogen deprivation.
ALI16285 ALI16285.1 GI:5831501
cDNA library; nitrogen deprivation.
BOLTYOLINIA fluckellana.
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BOLTYLIS cinerea strain T4 cDNA library under conditions of nitrogen deprivation.
ALI10729
ALI10729.1 GI:5825016
BOLTYOCHINA fuckeliana.
BOLTYOCHINA fuckeliana.
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/note="Genoscope sequence ID : W33E081"
120 c 133 g 135 t
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/organism="Botryotinia fuckeliana"
 Score 13.2; DB 14;
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Matches 12; Conservative
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19 ACTCCAAGCACTCCA 33
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Submitted (01-SEP-1999) Genoscope - Centre National de Sequencage :
CP 5706 91057 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
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The cDNA library to be analyzed within the framework of this project was created using a Botrytis cinerea strain which was grown under conditions of nitrogen deprivation, which is the normal situation for B. cinerea during its development on its host plant. The library was produced in an oriented direction, in the pBSII
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1 (bases I to 540)
Bliton, F., Levis, C., Fortini, D., Pradier, J.M. and Brygoo, Y. Direct Submission
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121 c 128 g 135 t
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Pred. No. 2.1e+03;
2; Mismatches 1;
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Kelly, P.A. and Nagano, M.
Soluble human prolactin receptors
Patent: US 6083753-A 3 04-JUL-2000;
Location/Qualifiers
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Botryotinia fuckeliana.
Botryotinia fuckeliana
                                                                                                               AR102280 357 bp DNA
Sequence 3 from patent US 6083753.
AR102280
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90 c 76 g
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317 ACTCCATGCACTCCA 303
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25-MAY-1999

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2 (bases 1 to 172)
Hu,Z.Z., Zhuang,L., Meng,J.P. and Dufau,M.L.
Direct Submission
Submitted (16-SEP-1998) ERRB, NICHD, 9000 Rockville Pike, Bethesda,
MD 20892, USA
                                                                                                                                                                                                   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhin; Hominidae; Homo.
1 (bases 1 to 172)
Hu,Z.Z., Zhuang,L., Meng,J., Leondires,M. and Dufau,M.L.
The human prolactin receptor gene structure and alternative .
promoter utilization: the generic promoter hPIII and a novel human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 13.2; DB 93; Length 172; Pred. No. 2.2e+03; 2; Mismatches 1; Indels 0.
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                                                                                                                                                                                                                                                                                                                promoter hP(N)
J. Clin. Endocrinol. Metab. 84 (3), 1153-1156 (1999)
99182102
                                                                          HSPLR07 172 bp DNA PRI
Homo sapiens prolactin receptor gene, exon 7.
AF091867.1 GI:4886763
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1 (bases 1 to 357)

Kelly P.N. and Nagano, M.
Soluble human prolactin receptors
Patent: US 6083714-A 3 04-JUL-2000;
Location/Qualifiers
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Sequence 3 from patent US 6083714.
AR101840 GI:12812638
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AR101845 Sequence
AR102285 Sequence
AL411034 T7 end of
AX010400 Sequence
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M60329 Cow beta-A2
AF166331 Homo sapi
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AF081273 Bos tauru
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L05561 Arabidopsis
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AF349939 Homo sapi
U03413 Dictyosteli
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D89016 Homo sapien
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A86031 Sequence 69
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Pred. No. 2.2e+03;
2; Mismatches 1; Indels
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M unidentified.

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1 (bases 1 to 108)

Haseloff,J.P. and Hodge,S.

IMPROVEMENTS IN OR RELATING TO GENE EXPRESSION
Patent: WO 9730164-A 6 21-AuG-1997;

MEDICAL RES COUNCIL (GB)

Other publication AU 1801497 19970902.
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/db_xref="taxon:32644"
25 c 46 g 19
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Sequence 6 from Patent WO9730164.
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Soluble human prolactin receptor (hPRLR) isoforms have been isolated from the human gastrointestinal tract. The isoforms have a deletion in the extra- or intracellular domain and are thought to be generated by alternative splicing, since four clones (A. B. C and E) precisely lack one or two exons. Except for clone C, the deletion in all other clones resulted in a frameshift and produced a stop codon before the transmembrane domain. The soluble hPRLR may be used as a binding protein for human prolactin and/or human growth hormone, which can be used in diagnostics for the detection and measurament of the binding ligand or in the rappeutics for binding to human prolactin and/or human growth hormone to retard or inhibit their hormone activities. They may also be used in the ceptor and inthodies to provide solution-based radioligand receptor assays, in receptor sandwich or enzymatic assays, and in X-ray crystallographic analysis to develop molecular models, which define the certiary structure of the hormone-binding domains, where such information would provide insight into the structure of the actual contact between a hormone and its receptor. This structure information would be useful in the design of peptides which have prolactin or growth hormone-like
                                                                                                                                                                                                                                                                                                              New soluble prolactin receptors useful as human growth hormone binding protein and in x-ray crystallographic analysis for developing molecular models which define the tertlary structure of the hormone-binding
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Pred. No. 3.3e+02;
2; Mismatches 1; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAA49977 standard; cDNA; 357 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         88.0%;
80.0%;
                                                                           97US-0806597.
                                                                                                                  96us-0012503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                317 ACTCCATGCACTCCA 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag=
73..354
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Best Local Similarity
                                                                                                                                                                                                                    Kelly PA, Nagano M;
                                                                                                                                                                                                                                                       WPI; 2000-464339/40.
P-PSDB; AAY96916.
                                                                           26-FEB-1997;
                                                                                                                  29-FEB-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                    04-JUL-2000
US6083714-A
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                                                                                                                                                                                                                                                                                                                                                                            domains
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The present sequence is that of DNA encoding a newly identified soluble isoform of the human prolactin receptor (PRLR). The DNA lacks exons 5 and 6 of the full-length receptor, resulting in a lacks exons 5 and 6 of the full-length receptor, resulting in a saking the putative protein product (see AAY95524) a secreted form of the receptor. 6 Isoforms (see AAA997682) of human PRLR were identified in human colonic Cacco 2 and human breast cancer T-47D cells. Recombinant DNA molecules encoding the soluble PRLRs are provided, as well as expression vectors and host cells. The soluble PRLRs may be used as binding proteins for human prolactin and/or human growth hormone, which can be useful in diagnostics for the detection and measurement of the binding ligand, or in therapeutics for binding to human prolactin and/or human growth hormone activities. They may also be used in place of inhibit their hormone activities. They may also be used in place of inhibit their hormone activities. They may also be used in place of inhibit their hormone activities.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New recombinant DNA having a segment encoding a signal peptide joined translationally to a segment encoding a soluble human prolactin receptor useful as a hormone growth hormone binding protein, and in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            such information would provide insight into the structure of the actual contact between a hormone and its receptor. This structural information would be useful in the design of peptides that have
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               prolactin or growth hormone-like agonistic or antagonistic activity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 x-ray crystallographic analysis
                                                                                                                                                                          97US-097042B
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Best Local Similarity 80.0
Matches 12; Conservative
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                                                                                                                                                                          14-NOV-1997;
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26-FEB-1997;
US6083753-A.
                                                                                     04-JUL-2000.
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1 RCTCCANGCRCTCCA 15
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                                                                                   Chlamydia pneumoniae.
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6 gctccaagcactcca
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                                                                                                                                                                                    (GEST ) GENSET
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                                                                                                                                        20-NOV-1998;
                                                                                                                                                         04-NOV-1998;
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                                                                                                                                                                                                      Griffais R;
                                                                         Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAA53588;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           as binding to the proteins are used for the treatment of such disorders.
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           Length 15;
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                            Indels
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                                                                                                                                                                                   Haemopoietin receptor family; NR8; antibody; diagnosis; blood formation disorder; fusion protein; probe; ss.
         Score 13.2; ·DB 21;
Pred. No. 2.6e+02;
2; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 13.2; DB 21;
Pred. No. 2.6e+02;
                                                                                                                                                                                                                                                                                                                 (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 15 BP; 3 A; 1 C; 7 G; 4 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Mismatches
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                                                                                                          AAZ90895 standard; DNA; 15 BP.
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80.0%;
         88.0%;
80.0%;
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98JP-0297409.
                                                                                                                                               (first entry)
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                                                                                                                                                                  Human NR8 gene probe #123.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 88.0
Best Local Similarity 80.0
Matches 12; Conservative
                            Conservative
                                             1 RCTCCANGCRCTCCA 15
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15 ACTCCATGCACTCCA 1
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15 ACTCCATGCACTCCA
Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                    Maeda M;
                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                WO9967290-A1
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19-OCT-1998;
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                                                                                                                             AAZ90895;
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                                                                                           RESULT 12
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AAX91991-X97517 represent PCR primers used to amplify open reading frames and other nucleic acid sequences from the genome of chlamydia pneumoniae (see AAX91940). C. pneumoniae causes respiratory disease such as pneumonia and bronchitis and is thought to be a contributing factor in heart disease, sarcoidosis, sinusitis, purulent otitis media, erythema endosum or pharynquitis. The polypeptides encoded by the open reading frames of the C. pneumoniae genome (see AAY34581-Containing C. pneumoniae nucleotides sequences containing C. pneumoniae, especially where the vector directs the expression of a neutralising epitope of C. pneumoniae.
                                                                     Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis; sinusitis; purulent otitis media; erythema nodosum; pharyngitis; vaccine; neutralising epitope; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hPRLR; soluble; prolactin receptor; gastrointestinal; splice variant; binding protein; prolactin; growth hormone; agonist; antagonist; ss.
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PCR primer used to amplify an ORF of Chlamydia pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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80.0%; Pred. No. 2.7e+02;
iive 2; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 20 BP; 7 A; 8 C; 3 G; 2 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genome sequence of Chlamydia pneumoniae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Page 1496; Disclosure; 1912pp; English.
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97FR-0014673.
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les 12; Conservative
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Length 15; Indels

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the amino acid sequence Trp-Ser-Xaa-Trp-Ser. The sequences Assasses 8:59300 and AA290816-290925 represent specific examples of probe sequences used in the search. Antibodies to the NRB family proteins are used for the diagnosis of blood formation disorders. Compounds identified
                                                                                                                                                as binding to the proteins are used for the treatment of such disorders.
                                      The invention relates to the isolation of sequences encoding human haemopoietin receptor protein family NR8 genes. The NR8 family sequences were initially searched for comparison on a nucleic acid database with the nucleic acid probe sequence TGGAGYNNNTGGAGY encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hemopoletin receptor protein family NRB used for diagnosis of blood
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                                                                                                                                                                                                                88.0%; Score 13.2; DB 21;
80.0%; Pred. No. 2.6e+02;
ive 2; Mismatches 1;
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                                                                                                                                                                           Sequence 15 BP; 2 A; 2 C; 7 G; 4 T; 0 other;
             Example 1; Page 43; 176pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                 AAZ90883 standard; DNA; 15 BP
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98JP-0297409
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Matches 12; Conservative
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                                                                                                                                                                                                                                                                                     formation disorders -
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                                                                                                                                                                                                                                                                                                                                                                                            AAZ90883;
                                                                                                                                                                                                                   Query Match
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                                                                                                                                                                                                                                                      The invention relates to the isolation of sequences encoding human haemopoletin receptor protein family NR8 genes. The NR8 family sequences were initially searched for comparison on a nucleic acid database with the nucleic acid probe sequence TGGAGYINNTGGAGY encoding the amino acid sequence Trp-Ser-Xaa-Trp-Ser. The sequences AALS9258-259300 and AA290416-290925 represent specific examples of probe sequences used in the search. Antibodies to the NR8 family proteins are used for the diagnosis of blood formation disorders. Compounds identified as binding to the proteins are used for the treatment of such disorders.
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                                                                                                                                                                                   Hemopoletin receptor protein family NR8 used for diagnosis of blood formation disorders - \,
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                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 13.2; DB 21 Pred. No. 2.6e+02;
                                                                                                        (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
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                                                                                                                                                                                                                              Example 1; Page 42; 176pp; Japanese.
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80.0%;
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98JP-0297409.
                                      99WO-JP03351
                                                                 98JP-0214720
                                                                             98JP-0297409
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human NRB gene probe #105
                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 88.0
Best Local Similarity 80.0
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 RCTCCANGCRCTCCA 15
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15 ACTCCAGGCACTCCA 1
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                                                                                                                                                             WPI; 2000-116933/10.
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                                                                                                                                    Maeda M;
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                                      23-JUN-1999;
                                                                             19-OCT-1998;
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            29-DEC-1999
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The invention relates to the isolation of sequences encoding human haemopoietin receptor protein family NRB genes. The NRB family sequences were initially searched for comparison on a nucleic acid database with the nucleic acid probe sequence TGGAGYNNNTGGAGY encoding the amino acid sequence Trp-Ser-Xaa-Trp-Ser. The sequences AALS928B-259300 and AALS9016-290925 represent specific examples of probe sequences used in the search. Antibodies to the NRB family proteins are used for the diagnosis of blood formation disorders. Compounds identified as binding to the proteins are used for the treatment of such disorders.
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Example 1; Page 43; 176pp; Japanese.
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us-09-532-263-8.rng

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24 - MAY - 2000
                                                                                                                                            Homo sapiens
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                                            AAZ90861;
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ID AAZ908
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            AAZ90861/c
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sequences used in the search. Antibodies to the NRB family proteins are used for the diagnosis of blood formation disorders. Compounds identified as binding to the proteins are used for the treatment of such disorders.
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0
                                                                           Length 15;
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                                                                                                Indels
                                                                                                                                                                                                                                                                                  Haemopoietin receptor family; NR8; antibody; diagnosis; blood formation disorder; fusion protein; probe; ss.
                                                                         Score 13.2; DB 21;
Pred. No. 2.6e+02;
2; Mismatches 1;
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Pred. No. 2.6e+02;
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                                          Sequence 15 BP; 3 A; 1 C; 7 G; 4 T; 0 other;
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                                                                                                                                                                                               BP.
                                                                          88.0%;
80.0%;
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80.0%;
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98JP-0297409.
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                                                                                                                                                                                          AAZ90837 standard; DNA; 15
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Matches 12; Conservative
                                                                         Query Match 88.0
Best Local Similarity 80.0
Matches 12; Conservative
                                                                                                                                                                                                                                                             Human NR8 gene probe #65
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15 ACTCCATGCACTCCA 1
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The invention relates to the isolation of sequences encoding human haemopoietin receptor protein family NR8 genes. The NR8 family sequences were initially searched for comparison on a nucleic acid database with the nucleic acid probe sequence TGGAGYNNNTGGAGY encoding the amino acid sequence Trp-Ser-Xaa-Trp-Ser. The sequences AAAS9258-259300 and AAS90816-290925 represent specific examples of probe sequences used in the search. Antibodies to the NR8 family proteins are used for the diagnosis of blood formation disorders. Compounds identified as binding to the proteins are used for the treatment of such disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hemopoietin receptor protein family NRB used for diagnosis of blood formation disorders - \,
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  BP.
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98JP-0297409
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AAZ90861 standard; DNA; 15
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les 12; Conservative
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15 ACTCCATGCACTCCA
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1 RCTCCANGCRCTCCA 15
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                           WPI; 2000-116933/10.
                                                         formation disorders
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          Maeda M;
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19-OCT-1998;
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          Nomura H,
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Matches 1
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  Db
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                                                                                                                                                                                                    protein family NRB used for diagnosis of blood
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        Haemopoietin receptor family; NR8; antibody; diagnosis;
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                  blood formation disorder; fusion protein; probe; ss.
                                                                                                                                                                                                                                                                                                                                                                          Score 13.2; DB 21;
Pred. No. 2.6e+02;
2; Mismatches 1;
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80.0%;
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                                                                                                                                                                                                                                                                                                                                                                                              12; Conservative
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                                                                                                                                                                                                   Hemopoletin receptor formation disorders -
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                                                                                                                                                               Maeda M;
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                                     Homo sapiens
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Hemopoietin receptor protein family NR8 used for diagnosis of blood
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80.0%; Pred. No. 2.6e+02;
.ive 2; Mismatches 1;
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                                                                                                                Example 1; Page 40; 176pp; Japanese.
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98JP-0297409
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Gaps

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Indels

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Mismatches

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12; Conservative

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              The invention relates to the isolation of sequences encoding human haemopoletin receptor protein family NR8 genes. The NR8 family sequences were initially searched for comparison on a nucleic acid database with the nucleic acid probe sequence TGGAGYINNTGGAGY encoding the amino acid sequence Trp-Ser-Xaa-Trp-Ser. The sequences AAZ$258~259300 and AAZ$00816~290925 represent specific examples of probe sequences used in the search. Antibodies to the NR8 family proteins are used for the diagnosis of blood formation disorders. Compounds identified as binding to the proteins are used for the treatment of such disorders.
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Pred. No. 2.6e+02;
2; Mismatches 1;
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80.0%;
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ID AAZ59267 standard; DNA; 15
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Best Local Similarity 80.0
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15 GCTCCAGGCACTCCA 1
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Length 15;

Score 13.2; DB 21; Pred. No. 2.6e+02;

88.0%; 80.0%;

Query Match Best Local Similarity

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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PS	Exa	Example	l; Page		38; 176pp;		Japanese.	

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                                                                                                                                                                                                                                                                                                  Email: genome-resertc.riken.go.jp
Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA (Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
Transcriptional sequencing: A method for DNA sequencing using RNA polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
Please visit our web site (http://genome.rtc.riken.go.jp) for
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Sato,K., Shibata,Y., Shigemoto,Y., Shiraki,T., Sogabe,Y., Sugahara,Y., Suzuki,H., Suzuki,H., Tateno,M., Tomaru,Y., Tominaga,N., Matanabe,S., Yagame,M., Yamamura,T., Yokota,T., Yoshino,M., Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.
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AV081754 Mus musculus stomach C57BL/6J adult Mus musculus CDNA
clone 2210421D01, mRNA sequence.
AV081754 GI:5213202
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/db_xref="taxon:10090"
/clone="2200005J24"
/clone_lib="Mus musculus stomach C57BL/6J adult"
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Tel: 81-298-36-9145
Fax: 81-298-36-9098
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Contact: Chie Owa
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Matches 12; Conservative
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Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length CDNA (Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
Transcriptional sequencing: A method for DNA sequencing using RNA polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
Transcriptional sequencing: A method for DNA sequencing using RNA please visit our web site (http://genome.rtc.riken.go.jp) for further details.

Location/Oualifiers

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Tel: 81-298-36-9145
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Fax: 81-298-36-9145
Fax: 81-298-36-9104
Final: genome-resertc.riken.go.jp
Thermostabilization and thermoactivation of thermolabile enzymes by
trehablose and its application for the synthesis of full length cDNA
(Proc. Natl. Acad. Sci. U.S. A. 95(2):520-524 (1998))
Transcriptional sequencing: A method for DNA sequencing using RNA
polymerase (Proc. Natl. Acad. Sci. U.S. A. 95(7):3455-3460 (1998))
Please visit our web site (http://genome.rtc.riken.go.jp) for
further details.
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Carningly P., Shibata, K., Ozawa, Y., Konno, H., Itoh, M., Aizawa, K., Akahira, S., Akiyama, J., Fukuda, S., Fukunishi, Y., Funayama, T., Hara, A., Hayatsu, N., Hori, F., Ishikawa, T., Itoh, M., Izawa, M., Kawal, J., Sikuchi, N., Kojima, Y., Matsuyama, T., Nitsuma, H., Oda, H., Owa, C., Sato, K., Shibata, Y., Shigamoto, Y., Shiraki, T., Sogabe, Y., Sugahara, Y., Suzuki, H., Tateno, M., Tomaru, Y., Tominaga, N., Watanabe, S., Yagame, M., Yamamura, T., Yokota, T., Yoshino, M.,
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Carninci,P., Shibata,K., Ozawa,Y., Konno,H., Itoh,M., Aizawa,K.,
Akahira,S., Akiyama,J., Fukuda,S., Fukunishi,Y., Funayama,T., Hara,A., Hayatsu,N., Hori,F., Ishikawa,T., Itoh,M., Izawa,M., Kawal,J.,
Kikuchi,N., Kojima,Y., Matsuyama,T., Niitsuma,H., Oda,H., Owa,C.,
                                                                                                                    Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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AV072658
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/clone_lib="Mus musculus stomach C57BL/6J adult"
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Pred. No. 4.8e+03;
2; Mismatches 1;
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  clone 2200005H20, mRNA sequence.
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/db_xref="taxon:10090"
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Genome Science Laboratory
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 173)

Raniars., Akiyama,7., Fukuda,S., Fukunishi,Y., Funayama,T., Hara,A., Hayatsu,N., Haribikawa,T., Itoh,M., Izawa,M., Hara,A., Rikuchi,N., Kojima,Y., Matsuyama,T., Niitsuma,H., Oda,H., Owa,C., Shapata,Y., Shigemoto,Y., Shigemoto,Y., Shigemoto,Y., Suzuki,H., Tateno,M., Tomaru,Y., Suguka,Y., Suzuki,H., Tateno,M., Tomaru,Y., Tominaga,N., Matanabe,S., Yagame,M., Yamamura,T., Yokota,T., Yoshino,M., RIKEN Mouse ESTS

Unpublished (1999)

Contact: Chie Owa

Genome Science Laboratory
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Score 13.2; DB 109; Length 171; Pred. No. 4.8e+03; 2; Mismatches 1; Indels 0;
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Fax: 81-298-36-9098
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/db_xref="taxon:10090"
/clone="2200007C09"
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/dev_stage="adult"
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                                                                                                                                                        (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymerase act and polymerase and T4 polymerase act and T4 polymerase act and T4 polymerase act and T4 polymerase to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (qi|4732114qb|AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Exail: genome-res@ttc.riken.go.jp
Thermostabilization and thermoactivation of thermolabile enzymes by
trehablose and its application for the synthesis of full length cDNA
(Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
Transcriptional sequencing: A method for DNA sequencing using RNA
polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
Please visit our web site (http://genome.rtc.riken.go.jp) for
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases I to 166)

Carninci, P., Shibata, K., Ozawa, Y., Konno, H., Itoh, M., Aizawa, K.,

Akahira, S., Akiyama, J., Eukudas, S., Eukunishi, Y., Funayama, T., Hara,

A., Hayatsu, N., Hori, F., Ishikawa, T., Itoh, M., Izawa, M., Kawai, J.,

Kikuchi, N., Kojima, Y., Matsuyama, T., Niitsuma, H., Oda, H., Owa, C.,

Sato, K., Shibata, Y., Shigemoto, Y., Shiraki, T., Sogabe, Y., Sugahara, Y., Suzuki, H., Tareno, M., Tomaru, Y., Tominaga, N.,

Matanabe, S., Yagame, M., Yamamura, T., Yokota, T., Yoshino, M.,

Muramattsu, M., Okazaki, Y. and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
0
                                                   /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AV073140 166 bp mRNA EST 24-JUN-1999
AV073140 Mus musculus stomach C57BL/6J adult Mus musculus CDNA
clone 2200008009, mRNA sequence.
AV073140
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Pred. No. 4.8e+03;
2; Mismatches 1; Indels 0;
'clone_lib="Mouse 10kb plasmid UUGC1M library"
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                                                                                                                                          Laboratory Mouse DNA Resource
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80.0%;
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Best Local Similarity 80.09
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Unpublished (1999)
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62 ACTCCAGGCACTCCA 48
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KEYWORDS
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1-1. Koyadai, Tsukuba, Ibaraki 305-0074, Japan Tel: 81-298-36-9145
Fax: 81-298-36-91045
Fax: 81-298-36-91045
Fax: 81-298-36-9104
Fax: 81-298-36-9104
Faxion and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA (Proc. Natl. Acad. Sci. U.S. A. 95(2):520-524 (1998))
Transcriptional sequencing: A method for DNA sequencing using RNA polymerase (Proc. Natl. Acad. Sci. U.S. A. 95(7):3455-3460 (1998))
Please visit our web site (http://genome.rtc.riken.go.jp) for further details.
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Carninci, P., Shibata, K., Ozawa, Y., Konno, H., Itoh, M., Alzawa, K., Akahira, S., Akiyama, J., Fukuda, S., Fukunishi, Y., Funayama, T., Hayatsu, N., Hayatsu, N., Hayatsu, N., Hayatsu, N., Shikawa, T., Itoh, M., Izawa, M., Kawai, J., Sato, K., Shibata, Y., Shigemoto, Y., Shiraki, T., Sogabe, Y., Sugahara, Y., Suzuki, H., Pateno, M., Pomaru, Y., Tominaga, N., Matamabe, S., Yagame, M., Yamamura, T., Yokota, T., Yoshino, M., Nexazaki, Y. and Hayashizaki, Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AV076989 1171 bp mRNA EST 24-JUN-1999 AV076989 Mus musculus stomach C57BL/6J adult Mus musculus CDNA clone 2210021D15, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
1. .166
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/db.zref="taxon:10090"
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/clone="1b"="Mus musculus stomach C57BL/6J adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="Mus musculus stomach C57BL/6J adult"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                            Score 13.2; DB 109; Length 166; Pred. No. 4.8e+03; 2; Mismatches 1; Indels 0;
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/organism="Mus musculus"
                                                                                                                                                                    /sex="male"
/tissue_type="stomach"
/dev_stage="adult"
49 c 33 g
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53 c 32 q
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1999)
Contact: Chie Owa
Genome Science Laboratory
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                                                                                                                                                                                                                                                                                                                                                                               88.0%;
80.0%;
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Best Local Similarity 80.0
Matches 12; Conservative
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us-09-532-263-8.rst

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/clone="UUGC1M0130J06"
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Matches 12; Conservative
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71 GCTCCATGCACTCCA 85
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1 (bases 1 to 162)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deolivelra, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                   Tail: 81-298-36-9145

Fax: 81-298-36-9098

Email: genome-resertc.riken.go.jp

Thermostabilization and thermoactivation of thermolabile enzymes by

trehalose and its application for the synthesis of full length cDNA

(Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))

Transcriptional sequencing: A method for DNA sequencing using RNA

polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))

Please visit our web site (http://genome.rtc.riken.go.jp) for

further details.
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Kikuchi, N., Kojima, Y., Matsuyama, T., Niitsuma, H., Oda, H., Owa, C., Sato, K., Shibata, Y., Shiqamoto, Y., Shiraki, T., Sogabe, Y., Sugahara, Y., Suzuki, H., Suzuki, H., Tateno, M., Tomaru, Y., Tominaga, N., Watanabe, S., Yagame, M., Yamamura, T., Yokota, T., Yoshino, M., Ruramatsu, M., Okazaki, Y. and Hayashizaki, Y.
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Shorgun sequencing of the human transcriptome with ORF expressed
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Mus musculus"
/strain="C57BL/6J"
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50 c 30 q
                                                                                                                                                   Contact: Chie Owa
Genome Science Laboratory
RIKEN
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Fax: +55-11-2707001
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44 ACTCCAGGCGCTCCA 58
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1...162
/organism="Homo sapiens"
/db_xerf="texton:9606"
/clone_lih="BT0389"
/dev_stage="Adult"
/clone_lih="br0389"
/dev_stage="Adult"
/note="Organ: breast; Vector: pucl8; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196
/716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

51 a 33 c 37 g 41 t
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=RC2-BT0389-090
300.012-f12&t3=2000-03-09&t4=1)
Seq primer: puc l8 forward
High quality sequence start: 44
High quality sequence start: 44
High quality sequence stop: 162.
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Wm. 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (Jass 1 to 164)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly
, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
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Pred. No. 4.7e+03;
2; Mismatches 1; Indels 0;
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error:
Plate: 0130 row: J column: 06
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/strain="C57BL/6J"
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Query Match
Best Local Similarity 80.0
Matches 12; Conservative
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42 ACTCCAGGCGCTCCA 56
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E 1 (bases 1 to 160)

S Carninci, P., Shibata, K., Ozawa, Y., Konno, H., Itoh, M., Aizawa, K., Akahira, S., Akipama, J., Fukuda, S., Fukudishi, Y., Funayama, T., Hara, A., Hayatsu, N., Hori, F., Ishikawa, T., Itoh, M., Isawa, M., Gwai, J., Kikuchi, N., Kojima, Y., Matsuyama, T., Itoh, M., Oda, H., Owa, C., Sato, K., Shibata, Y., Shiraki, Y., Shiraki, Y., Suzuki, H., Suzuki, H., Tateno, M., Tomaru, Y., Tominaga, N., Watanabe, S., Yagame, M., Yamamura, T., Yokota, T., Yoshino, M., RIKEN Mouse ESTS

L Unpublished (1999)

Contact: Chie Owa
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Transcriptional sequencing: A method for DNA sequencing using RNA polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))

Please visit our web site (http://genome.rtc.riken.go.jp) for
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             Score 13.2; DB 109; Length 159;
Pred. No. 4.7e+03;
2; Mismatches 1; Indels 0;
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Tel: 81-298-36-9145
Fax: 81-298-36-9098
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2; Mismatches 1;
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/organism="Mus musculus"
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/clone="2210009E18"
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49 c 29 g
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               Query Match 88.0
Best Local Similarity 80.0
Matches 12; Conservative
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Best Local Similarity 80.0
Matches 12; Conservative
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Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length CDNA (Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
Transcriptional sequencing: A method for DNA sequencing using RNA polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
Please visit our web site (http://genome.rtc.riken.go.jp) for
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AV074715 Mus musculus stomach C57BL/6J adult Mus musculus cDNA clone 2210010H07, mRNA sequence.
AV074715
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AV072831 Mus musculus stomach C57BL/6J adult Mus musculus cDNA
clone 2200006M08, mRNA sequence.
AV072831
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/sex="male"
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Pred. No. 4.7e+03;
2; Mismatches 1; Indels 0;
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Tel: 81-298-36-9145
Fax: 81-298-36-9098
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/strain="C578L/6J"
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/dev_stage="adult"
42 c 32 a
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Fax: 81-298-36-9098
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Contact: Chie Owa
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(Carninci, P., Shibata, K., Ozawa, Y., Konno, H., Itoh, M., Aizawa, K., Akahira, S., Akiyama, J., Fukuda, S., Fukunishi, Y., Funayama, T., Hara, Maraku, N., Hori, F., Ishikawa, T., Itoh, M., Izawa, M., Kawai, J., Kituchi, N., Kojima, Y., Matsuyama, T., Niitsuma, H., Oda, H., Owa, C., Sato, K., Shibata, Y., Shigemoto, Y., Shiraki, T., Sogabe, Y., Sugahara, Y., Suzuki, H., Suzuki, H., Yarateno, M., Tomaru, Y., Tominaga, N., Matanabe, S., Yagame, M., Yamamura, T., Yokota, T., Yoshino, M., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y.
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Transcriptional sequencing: A method for DNA sequencing using RNA polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
Please visit our web site (http://genome.rtc.riken.go.jp) for further details.
                                                                                                     Email: genome-resertc.riken.go.jp
Thermostabilization and thermoactivation of thermolabile enzymes by
trehalose and its application for the synthesis of full length cDNA
(Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
Transcriptional sequencing: A method for DNA sequencing using RNA
polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
Flease visit our web site (http://genome.rtc.riken.go.jp) for
further details.
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Pred. No. 4.7e+03;
2; Mismatches 1; Indels 0;
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Tel: 81-298-36-9145
Fax: 81-298-36-9098
                                     3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-9145
Fax: 81-298-36-9098
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Genome Science Laboratory
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Unpublished (1999)
Contact: Chie Owa
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Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA (Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
Transcriptional sequencing: A method for DNA sequencing using RNA polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
Please visit our web site (http://genome.rtc.riken.go.jp) for further details.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutherla; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 159)

Carninci, P., Shibata, K., Ozawa, Y., Konno, H., Itoh, M., Alzawa, K.,

Akahira, S., Akiyama, J., Fukuda, S., Fukunishi, Y., Funayama, T., Hara,

A., Hayatsu, N., Hori, F., Ishikawa, T., Itoh, M., Izawa, M., Kawai, J.,

Kikuchi, N., Kojima, Y., Matsuyama, T., Niitsuma, H., Oda, H., Owa, C.,

Sato, K., Shibata, Y., Shigemoto, Y., Shiraki, T., Sogabe, Y., Sugahara, Y., Suzuki, H., Suzuki, H., Yamamura, T., Yokota, T., Tominaga, N.,

Muramatsu, M., Okazaki, Y. and Hayashizaki, Y., Yoshino, M.,
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AV072952 Mus musculus stomach C57BL/6J adult Mus musculus CDNA
clone 2200007101, mRNA sequence.
AV072952
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80.0%; Pred. No. 4.7e+03;
iive 2; Mismatches 1;
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41 c 27 q
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51 c 27 q
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us-09-532-263-8.rst

Stamova,B. and Tong,J.C. The structure and function of the expressed bortion of the wheat	genomes - Early reproductive apex cDNA library from Triticum monococcum	Unpublished (2001) Coptact: Olin Anderson	US Department of Agriculture, Agriculture Research Service, Pacific West Arrae, Western Regional Research Center Agriculture and Agriculture Service, Pacific Buchanan Cream Albana, CA 04710, 100A	Tel: 5105595773 Fax: 5105595818	Email: oandersn@pw.usda.gov Sequence have been trimmed to remove vector sequence and low	score less than imer.	Location/Qualifiers 1119	/organism="Triticum monococcum" /cultivar="DV92"	/db_xref="taxon:4568" /clone="WHE2480_H02_004"	/clone_library" CDNA library"	/tissue_rype="Early reproductive apex" /dev_stage="Early reproductive apex" /lab hoct="E only wroto"	/note_Wector: Lambda Uni-ZAP XR, excised phagemid;	poly(A) RNA were prepared from apex at double-ridge stage	vegetative state to flower state, a CDNA library was made,	and the CDNA clones were in VIVO excised at the University of California, Davis (V. Echenique, B. Stamova	sequencing were performed in the OD Anderson lab (all	13 a 47 c 46 g 13 t		88.0%; Score 13.2; DB 155; Length 119; Similarity 80.0%; Pred. No. 4.7e+03;	vative 2; Mismato	1 RCTCCANGCRCTCCA 15 : :	rccargcactcca 83		AV080202 135 bp mRNA EST 25-JUN-1999 AV080202 Mus musculus stomach C57BL/6J adult Mus musculus cDNA	clone 2210413F10, mRNA sequence. AV080202	AV080202.1 GI:5211650 EST.	house mouse. Mus musculus	Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Euteleostoml; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	ır (mastsı 1 () 133) Garıninci,P., Shibata,K., Ozawa,Y., Konno,H., Itoh,M., Aizawa,K., Akahira,S., Akiyama,J., Fukuda,S., Fukunishi,Y., Funayama,T., Hara	A., Hayatsu,N., Hori,F., Ishikawa,T., Itoh,M., Izawa,M., Kawai,J., Kikuchi,N., Kojima,Y., Matsuvama,T., Niitsuma,H., Oda,H., Owa,C.	Sato, K., Shibata, Y., Shigemoto, Y., Shiraki, T., Sogabe, Y., Sugahara, Y., Suzuki, H., Suzuki, H., Tateno, M., Tomaru, Y., Tominaga, N., Watanabe, S., Yagame, M., Yamamura, T., Yokota, T., Yoshino, M.,	Muramatsu.M., Okazaki.Y. and Hayashizaki.Y. RIKEN Wouse ESTS Unpublished (1999) Contact: Chie Owa
TITLE		COMMENT					FEATURES Source										BASE COUNT	ORIGIN	Query Match Best Local	Matches		69	RESULT 2	NO	ACCESSION	-	SOURCE ORGANISM 1		AUTHORS		<u>-</u>	TITLE JOURNAL COMMENT
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		Description	BG607593 WHE2480_H AV080202 AV080202 AV081442	AV072952 AV072952 AV074451 AV074451			AV073140 AV073140 AV076989 AV076989	AV072630 AV072630	AV072658 AV072658 AV081754 AV081754	AV058439 AV058439 AL089661 Arabidops	AV077858 AV077851 AV077851 AV07258	AV073191 AV073191 AV077830 AV077830	BF145876 WHE1833_F AV072580 AV072580	AV072872 AV072872	AV072772 AV088929 AV072772 AV072772	AV072097 AV072097 AV073900 AV073900	AA840811 CFB32 Flo	BG141411 1838901.y BE670421 7e34h01.x AV072887 AV072887	AV072779 AV072779 AV072787 AV072787	AV072799 AV072799 AV074114 AV074114	AV072750 AV072750 AA319785 EST22073	AU071883 AU071883 AV288598 AV288598 AT618734 75450396	7480	1			17-APR-2001	early reproductive apex cDNA WHE2480_H02_O04, mRNA			; Embryophyta; Tracheophyta; da; Poales; Poaceae; Pooideae	Echenique,V., Han,P.S., Hsla Rausch,C.J., Seaton,C.L.,
SUMMARIES		B ID	155 BG607593 109 AV080202 109 AV081442														~	1/4 BG141411 138 BE670421 109 AV072887		109 AV072799 109 AV074114	- ₹	107 AUU/1883 28 AV288598 22 AT618724	9 AV0774 9 AV0783		ALIGNMENTS		bp mRNA	monococcum cDNA clone WHE2	57576	E	Triticum monococcum Eukaryota, Viridiplantae, Streptophyta, En Spermatophyta, Magnoliophyta, Liliopsida,	vsky,J., ller,R.,
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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gb_est39:*
gb_est40:*
                                                                                                                                                                                                                                                                                                                          EST:*
                                                                                                                          Perfect score:
                                                                                                                                                              Scoring table:
                                                                                                                                                                                                                                                                                                                         Database :
                                                                                                                                                                                              Searched:
                                                                                                                                       Sequence:
                                                                   Run on:
                                                                                                                 Title:
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em_estp18:* em_estp19:* em_estp110:*

em_estpl5:* em_estpl6:* em_estpl7:* em_estro2:*
em_estro3:*
em_estro4:*

em_estrol:

em_estro5:*
em_estro6:*
em_estro7:*

em_estro19:*
em_estro20:*
gb_est25:*
gb_est27:*
gb_est28:*
gb_est28:*
gb_est31:*
gb_est31:*
gb_est41:*
gb_est41:*
gb_est41:*
gb_est41:*
gb_est41:*
gb_est41:*

em_estro8:*
em_estro1:*
em_estro1:*
em_estro11:*
em_estro13:*
em_estro13:*
em_estro15:*
em_estro16:*
em_estro16:*
em_estro16:*
em_estro18:*

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BASE COUNT
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Lindahl,M., Timmusk,T., Rossi,J., Saarma,M. and Airaksinen,M.S. Expression and alternative splicing of mouse Gfra4 suggest roles in endocrine cell development
                                                                                                                                                                                                                                                                    /translation="MSTSSHACPVPAVRGHWTHYPAAPYPLLFPPVIRGLSLPPLHGL
HGHPPPSGCSTPSPASVGQACQRTTGGSQFAASTKWTPSLNAAIE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
Submitted (20-WAR-2000) Airaksinen M.S., Program in Molecular
Neurobiology, Institute of Biotechnology, P.O. Box 56 (Vilkinkaari
9), 00014 University of Helsinki, FINLAND
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AJ276872.1 GI:7688070 alternative splicing; GDNF family receptor alpha 4; Gfra4 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MMU276872 573 bp mRNA ROD 02-FEB-2001
Mus musculus mRNA for GDNF family receptor alpha 4, putative
                                                                                                                                                                   /codon_start=1
/product="retinoic acid receptor- beta 3 isoform"
/protein_id="Cna3921.1"
/db_xref="GI:53906"
/db_xref="MGD:MGI:97857"
/db_xref="SWISS-PROT:P22605"
                                                                                                                                                                                                                                                                                                                                     /product="retinoic acid receptor- beta 3 isoform"
446. .526
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 534;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 13.2; DB 94;
Pred. No. 1.7e+03;
2; Mismatches 1;
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/organism="Mus musculus"
/db_xref="taxon:10090"
/tissue_type="thyroid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       secreted isoform (Gfra4 gene).
/cell_line="F9, P19"
1. .534
                                                                                                                                                                                                                                                                                                                                                                                                                                                       135 g
                                                                                                                                                                                                                                                                                                      268. .>534
/gene="RAR-beta"
                                                                                                                                                                                                                                                                                                                                                                      /gene="RAR-beta"
                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="RAR-beta"
/note="exon 4"
                                                                    /gene="RAR-beta"
                                                                                                   /gene="RAR-beta"
                                                                                                                                                    /gene="RAR-beta"
                                    /gene="RAR-beta"
                                                                                                                                                                                                                                                                                                                                                                               /note="exon 2"
527. .>534
                                                                                                                   /note-"exon 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="Gfra4"
1. .573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       88.0%;
80.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 (bases 1 to 573)
Airaksinen, M.S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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387 ACTCCATGGGCTCCA 401
                                                                                    1. .445
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Mus musculus
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Best Local Similarity
Matches 12; Conserv
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20319126
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MMU276872/c
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KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                     BASE COUNT
ORIGIN
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AUTHORS
TITLE
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JOURNAL
                                                                                                                                                                                                                                                                                                                                                      exon
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/gene="Grans" in the short stands in the short stands in the short stands in the separating exons II and III"
//ocdon_start=1
//codouct="putative GDNF family receptor alpha 4, secreted isoform" // protein_id="CAB89692.1"
//db_xref="G1768801.09JJT2"
//translation="MAHCMESALLLLLIGSASFTDGNRCVDAREACTADERCQOLRS EXTREMBL:09JJT2"
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//translation="MAHCMESALLLLLIGSASFTDGNRCVDAREACTADERCGGSACAER RACTERPRACARSGRGGNERCREGUSRCR
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See also X56569, X56573, X56574 for Murine RAR-beta isoforms. Data kindly reviewed (18-FEB-1991) by Chambon P. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          X56574.1 GI:53905
RAR-beta gene; retinoic acid receptor; retinoic acid receptor beta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (Nov-1990) Chambon P., IGME/CRNS- U184/INSERM - Institute de Chimie Biologique, 11 rue Humann, 67085
STRASBOURG-Cedex, France
(bases 1 to 534)
Zelent,A., Mendelsohn,C., Kastner,P., Krust,A., Garnier,J.M.,
Differentially expressed isoforms of the mouse retinoic acid receptor beta generated by usage of two promoters and alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 534)
Chambon, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MMRARB3 534 bp mRNA ROD 16-APR-1991
Mouse RAR-beta mRNA for retinoic acid receptor-beta 3 isoform.
X56574
                                                                                                                                                                                                                                                                                                                      BAC end sequences from L. Hood at University of Washington. Designed and developed at the Stanford Human Genome Center. Location/Qualifiers
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 60 degrees C for 30 seconds
72 degrees C for 23 seconds
30
Perkin Elmer 9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 477;
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                                                                                                                             each 200 um
0.07 units/ul
5 ul
                                                                                                25 ng
each 1 uM
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Pred. No. 1.7e+03;
2; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121
                                                                                                                                                     Polymerase:
                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
/map="16"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1. .534
/organism="Mus musculus"
/db_xref="taxon:10090"
                                                                                                                                                                                                                          2.5 mM
50 mM
10 mM
8.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(267. .286)
131 c 112 g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="Human"
82. .286
 Annealing:
Polymerization:
                                       PCR Cycles:
Thermal Cycler:
                                                                                                                                                 Amplifaq Gold
Total Vol:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        88.0%;
80.0%;
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Best Local Similarity 80.0
Matches 12; Conservative
                                                                                                                                                                                                                                                               Tris-HCl:
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142 GCTCCAGGGACTCCA 156
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                                                                                              remplate:
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                                                                              Protocol:
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primer_bind
BASE COUNT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
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                                                                      Echinometra.
1 (bases 1 to 450)
Palumbi,S.R., Grabowski,G., Duda,T., Geyer,L. and Tachino,N.
Speciation and population genetic structure in tropical Pacific sea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="HPEVYILLLPGFGMISHVIAHYSGKREPFGYLGMVYAMIAIGVL
GGVWAHHMFTVGMDVDTRAXXAATMIIAVPTGIKVFSWMAXLQGSNLOWETPLFWA
LGFVFLFTLGGLTGGVYANSSIDVLHDTYXVVAHFHYVXSMGAVFAI"
103 93 9 125 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 477)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    G36845 477 bp DNA STS 31-DEC-1997 SHGC-60507 Human Homo sapiens STS genomic, sequence tagged site.
Echinometra mathaei.
Mitochondino Echinometra mathaei
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinosea; Echinoida; Echinometridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                               Evolution 51 (5), 1506-1517 (1997)
2 (bases 1 to 450)
Palumbi,S.R., Grabowski,G., Duda,T., Geyer,L. and Tachino,N. Direct Submission
Submitted (12-AGC-1997) OEB, Harvard University, 16 Divinity Avenue, Cambridge, MA 02138, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Initial incubation: 95 degrees C for 10 minutes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Stanford Human Genome Center (SHGC)
Stanford University School of Medicine
Department of Genetics, M-344, Stanford, CA 94305, USA
THE: 4157259689
Fax: 4157259689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 13.2; DB 5; Length 450;
Pred. No. 1.7e+03;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                             /codon_start=1
/transl_table=9
/product="cytochrome oxidase subunit I"
/protein_id="AAB69575.1"
/db_xref="GI:2353672"
                                                                                                                                                                                                                                                                                                                    /organism="Echinometra mathaei"
/organelle="mitochondrion"
/isolate="Nm4"
                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:31178"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: myers@shgc.stanford.edu
Primer A: GCTGCCGACAGACAGTTTG
Primer B: ATGCAGCATGAAGCATGGAG
STS size: 205
PCR Profile:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Richard M. Myers
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80.0%;
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Unpublished (1997)
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137 ACTCCAAGGACTCCA 123
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Matches 12; Conserv
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/gene="cask"
/gene="cask"
/gene="cask"
/gene="cask"
/codou_start=3
/product="calcium-sensing receptor"
/product="calcium-sensing receptor"
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AVEVIALLASFGLLACIFPNKYYIILEKPSNATIEEVRCSTAAHAFKVAARATLRRS
AVEVIALLASFGLSSSNASSKNSEDPFPQP"
149 c 103 g 82 t
                                                                                                                                                                                                                                                            AF221064 413 bp mRNA ROD 07-MAR-2000
Meriones unguiculatus calcium-sensing receptor (CaSR) mRNA, partial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AF018838 450 bp DNA INV 05-MAR-2001
Echinometra mathaei isolate NM4 cytochrome oxidase subunit I gene,
partial cds; mitochondrial gene for mitochondrial product.
AF018838 GT:2353671
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Gerbillinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wangemenn, P. and Scofield, M.A.
Direct Submission
Submitted (04-JAN-2000) Pharmacology, Creighton University, 2500
California Plaza, Omaha, NE 68178, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 413)
Nonneberger, K., Scofield, M.A. and Wangemann, P.
Evidence for a calcium sensing receptor in the vascular smooth muscle cells of the spiral modiolar artery
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/db_xref="taxon:10047"
/tissue_type="spiral modiolar artery; kidney"
<1. .>413
                                                                    Length 396;
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Pred. No. 1.8e+03;
2; Mismatches 1.
                                                                   Score 13.2; DB 97
Pred. No. 1.8e+03;
2; Mismatches 1
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AF221064.1 GI:7188643
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121 ACTCCATGGACTCCA 107
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/protein.id="AAA16747.1"
/db_xref="G1:404797"
/translation="MG10GGSVLFGLLLVLAVFCHSGNSLQCYSCPLPTMESMECTAS
TNCTSNLDSGLIARAGGSVYYRCWRFDDCSFKRISNQLSETQLKYTHCKNLCNVKEV
LENGGTTLSKKTILLLVTPFLAAAWSRHP"
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Mammalia, Eutheria, Primates, Platyrrhini, Cebidae, Cebinae,
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Rother, R.P., Rollins, S.A., Fodor, W.L., Albrecht, J.C., Setter, E.,

Fleckenstein, B. and Squinto, S.P.

Inhibition of complement-mediated cytolysis by the terminal

complement inhibitor of herpesvirus saimiri

J. Virol. 68 (2), 730-737 (1994)
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Saimiri sciureus complement regulatory protein (CD59) mRNA,
Complete cds.
L22859
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Pred. No. 1.8e+03;
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                                                                                                                                                                                                                                     (bases 1 to 396)
Fodor, W.L., Rollins, S. and Squinto, S.P.
Chimeric complement inhibitor proteins
Patent: US 5627264-A 6 06-MAY-1997;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Saimiri sciureus"
/db_xref="taxon:9521"
/cell_line="DPSO 114/74"
/tissue_type="lung"
/tissue_llb="ATCC CCL194"
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Sequence 6 from patent US 5627264.
149083
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Salmiri sciureus.
Salmiri sciureus
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96 c 95 g
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80.0%;
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121 ACTCCATGGACTCCA 107
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1 (bases 1 to 396)
Fodor, W.L., Rollins, S. and Squinto, S.P.
Fodor, W.L., Rollins, C. and Squinto, S.P.
Nucleic acid encoding chimeric complement inhibitor proteins
Patent: US 5624837-A 6 29-APR-1997;
Location/Qualifiers
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Rother, R., Rollins, S. and Squinto, S. P.
Terminal complement inhibitor fusion proteins
Patent: US 5847082-A 3 08-DEC-1998;
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Pred. No. 1.8e+03;
2; Mismatches 1;
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Pred. No. 1.8e+03;
2; Mismatches 1;
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Sequence 3 from patent US 5847082.
AROG4381
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Sequence 6 from patent US 5624837.
141335
141335.1 GI:2081925
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96 c 95 q
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96 c 95 g
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                  317. .>360
/gene="RAR-beta"
/note="exon 4"
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Best Local Similarity 80.0
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258 ACTCCATGGGCTCCA 272
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121 ACTCCATGGACTCCA 107
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KEYWORDS
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                   exon
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/db_xref="SWISS-PROT:P22605"
/translation="MSTSSHACPVPAVRGHWTHYPAAPYPLLFPPVIRGLSLPPLHGL
                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                X56569
X56569.1 GI:53901
RAR-beta gene; retinoic acid receptor; retinoic acid receptor beta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   See also X56569, X56573, X56574 for Murine RAR-beta isoforms. Data kindly reviewed (18-FEB-1991) by Chambon P. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 (bases 1 to 360)
Zelent,A., Mendelsohn,C., Kastner,P., Krust,A., Garnier,J.M.,
Ruffenach,F., Leroy,P. and Chambon,P.
Differentially expressed isoforms of the mouse retinoic acid
receptor beta generated by usage of two promoters and alternative
                                                                                                                                                                                                                                                                                                                                                   MMRARBI 360 bp mRNA ROD 16-APR-1991
Mouse RAR-beta mRNA for retinoic acid receptor-beta 1 isoform.
                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (08-NOV-1990) Chambon P., IGME/CRNS- U184/INSERM
Institute de Chimie Biologique, 11 rue Humann, 67085
STRASBOURG-Cedex, France
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              product="retinoic acid receptor- beta 1 isoform"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       product="retinoic acid receptor- beta 1 isoform"
protein_id="CAA39918.1"
/db_xref="GI:53902"
                                                                                                                                                                                                        ö
                                                                                                                                                                         Length 325;
                                                                                                                                                                                                          Indels

    .325
    /organism="Drosophila melanogaster"
/strain="Oregon R"
    /db_xref="taxon:7227"
    /clone="128B5"

                                                                                                                                                                       Score 13.2; DB 54;
Pred. No. 1.8e+03;
2; Mismatches 1;
                                                                                                           u
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1. 360
/organism="Mus musculus"
/db_xref="taxon:10090"
/chromosome="14A"
/cell_line="F9, p19"
date_of_search = 15-12-1995.
   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBO J. 10 (1), 71-81 (1991)
                                                                                                          75 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene="RAR-beta"
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/gene="RAR-beta"
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/gene="RAR-beta"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="RAR-beta"
/note="exon 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /codon_start=1
                                                                                                                                                                       88.0%;
80.0%;
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                                                                                                           2 9 L
                                                                                                                                                                                                        Conservative
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121 ACTCCATGGGCTCCA 135
                                                                                                                                                                                                                                      1 RCTCCANGGRCTCCA 15
                                                                                                                                                                       Query Match
Best Local Similarity
Matches 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                    house mouse.
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ORIGIN
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REFERENCE

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AUTHORS

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FEATURES

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RESULT MMRARB1

Dp ŝ

VERSION KEYWORDS

SOURCE

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Euruit fly.
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pteryota; Neoptera; Endopteryota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

[ pases 1 to 325)
European Drosophila Mapping, Consortium.
Direct Submission
Submitted (15-APR-1996) Michael Ashburner, Department of Genetics,
Downing St., Cambridge CB2 3EH, England
STS_name = Dm128B5S
CCIONE_NAME = 128B5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       D. melanogaster STS determined from European Mapping Project cosmid, sequence tagged site.
                                                                      14-NOV-1994 JP 1994278841
OTA YOSHIMI, ANAGUCHI HIROYUKI
C12N15/09,C07H21/04,C07K14/715,C12N1/21,C12P21/02,(C12N1/21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   database_searched = EMBL
database_version = 45.0 and updates till date_of_search
date_of_search = 08-01-1996
BLAST_program = BLASTX
database_searched = SWISSPROT
database_version = 32.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 324;
                                                                                                                                                                                                                                                 /organism="Mus sp."
/clone="pMALP-mBC"
1. 324
/product="mouse ligand-binding region
protein(BC) of G-CSF
receptor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 324 BP; 63 A; 103 C; 89 G; 69 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 13.2; DB 45;
Pred. No. 1.8e+03;
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                                                                                                                                                                                                            Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:10095"
                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Mus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       origin_of_clone = Oregon=R
in_situ_site_primary = 54F
BLAST_program = BLASTN
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TANPAKU KOGAKU KENKYUSHO:KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             88.0%;
80.0%;
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Z71056.1 GI:1263558
                                                                                                                                               strandedness: Double;
topology: Linear;
hypothetical: No;
                                                                                                                                    (C12P21/02,C12R1:19);
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Best Local Similarity 80.0
Matches 12; Conservative
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294 GCTCCAGGGGCTCCA 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 RCTCCANGGRCTCCA 15
                              Mus sp. (mouse)
JP 1996131172-A/3
                                                                                                                                                                                              anti-sense: No;
                                                            28-MAY-1996
                                                                                                                                                                                                                                                                                     mat_peptide
                                                                                                                      C12R1:19
                                                                                                                                                                                                                                         source
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DM128B5S
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                              COMMENT
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
Eutheria; Rođentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cDNA encoding mouse ligand-binding region protein(BC) of G-CSF receptor.
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"DNA CODING PROTEIN BC IN LIGAND-BOUND REGION IN GRANULOCYTE COLONY
"STIMULATING FACTOR RECEPTOR";
Patent number JP1996131172-A/3, 28-MAY-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                   Prepared with primer pairs derived from 238906 -- dbEST.
Location/Qualifiers
1. .310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 310;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
9 Cambridge Center, Cambridge MA 02142 USA
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Pred. No. 1.8e+03;
2; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-0CT-1997 (Rel. 52, Created)
02-SEP-2000 (Rel. 65, Last updated, Version 2)
                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens" 33, 539 33, 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          81
                                                                                                                                                                                                                                                                                  Tag Polymerase: 0.025 units/ul
                                           Email: thudson@genome.wi.mit.edu
                                                                        Primer A: AAAACAAAAACGCGATGA
Primer B: CCTTGACCCACCTTGAGAGA
STS size: 277
PCR Profile:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 standard; RNA; ROD; 324 BP.
                                                                                                                                               Denaturation:
Annealing: 56 degrees C
Polymerization:
PCR Cycles: 35
Thermal Cycler:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(290.
                                                                                                                                                                                                                                                         젎
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   88.0%;
80.0%;
                                                                                                                                                                                                                                      Template: 10 ng
Primer: each 5 ph
dNTPs: each 4 nM
                                                                                                                                                                                                                                                                                                                                         MgCl2: 1.5 mM
KCl: 50 mM
Tris-HCL: 10 mM
                                                                                                                                                                                                                                                                                                 Total Vol: 20 ul
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            Tel: 617 252 1900
Fax: 617 252 1902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12; Conservative
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211 ACTCCAGGGGCTCCA 225
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Best Local Similarity
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                                                                                                                                                                                                                            Protocol |
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ID E11372
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Gaps

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14-APR-2000

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Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates;
                                                                                                                                                                                                                                                                                                                          Submitted (05-JUN-1997) to the DDBJ/EMBL/GenBank databases. Hidekatsu Yoshioka, Okayama University Medical School, Molecular Biology and Biochemistry; 2-5-1 Shikata-cho, Okayama, Okayama 700, Japan (E-mail.mbb@ccews.cc.okayama-u.ac.jp, Tel:086-235-7128, Fax:086-222-7768)
                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                      1 (Sites)
Mahadazzaman,M., Sumiyoshi,H., Ueki,Y., Inoguchi,K., Ninomiya,Y.
and Yoshioka,H.
Structure of the human type XIX collagen (COL19A1) gene, which
suggests it has arisen from an ancestor gene of the FACIT family
Genomics 45 (2), 304-312 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Whitehead Institute/MIT Center for Genome Research; Physically
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STS sequence; primer; sequence tagged site.
human STSs derived from sequences in dbEST and the Unigene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 13.2; DB 85; Length 84; Pred. No. 2e+03; 2; Mismatches 1; Indels (
                                           ABOO468S29 84 bp DNA PRI 1
Human gene for Type XIX collagen al chain, exon 29.
ABOO4603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Thomas Hudson
Whitehead Institute/MIT Center for Genome Research
Whitehead Institute for Biomedical Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24
                                                                                                                                                                                                                                                                                                                                                                                                            1. .84
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="MKG34"
                                                                                                                                     Homo sapiens DNA, clone:MKG34.
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Catarrhini, Hominidae; Homo.
1 (bases 1 to 310)
Hudson, T.
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                                                                                    AB004603.1 GI:2598694
Type XIX collagen al chain.
29 of 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="COL19A1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           88.0%;
80.0%;
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human STS WI-6896.
G06299
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                                                                                                                                                                                                                                                                                 2 (bases 1 to 84)
Yoshioka, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              :||||| ||:|||||
46 ACTCCAGGGACTCCA 60
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                            RESULT 2
AB00468S29
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                                                                  DEFINITION
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AUTHORS
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G06299
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                                     AF018838 Echinomet
G36845. SHGC 60507
X56574 Mouse RAR-b
AJ276515 Mus muscu
AJ276515 Mus muscu
E09856 CDNA encodi
E11370 CDNA encodi
AF305546 Aspergill
AC057116 Giardia i
E11423 DNA encodin
M79325 MXXCCOCCUS
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AX06819 Sequence
AX068119 Sequence
AX090391 Sequence
S70577 RAR beta 1/
AJ276514 Mus muscu
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AJ276871 Mus muscu
AJ276516 Mus muscu
Y14605 Bos taurus
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AL400931 T7 end of
E11419 CDNA encodi
AL432214 T7 end of
AL422933 T3 end of
AF334165 Mycobacte
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/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Synthetic Oligonucleotide"
8 c 10 g 2 t
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Pred. No. 2.2e+03;
2; Mismatches 1;
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Ret ligand 5 (ret15) from human and mouse
Patent: WO 0116169-A 10 08-MAR-2001;
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MMU276872
MMU276515
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Location/Qualifiers
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80.0%;
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Best Local Similarity 80.0
Matches 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JOURNAL
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19-0CT-1995

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Sequence:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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        GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                       1344157 seqs, 7733874588 residues
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Maximum Match 100%
Listing first 45 summaries
                                          OM nucleic - nucleic search, using sw model
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1 RCTCCANGGRCTCCA 15
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Maximum DB seq length: 2000000000
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em_bh:*
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AX090397 Sequence AB004663 Human gen G06299 human STS W E11372 cDNA encodi Z71056 D. melanoga XS6569 Mouse RAR-b AR064381 Sequence I41335 Sequence

AX090397 AB00468S29 G06299 E11372 DM128B5S MMRARB1 AR064381

324 325 360 396 396

Description

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SUMMARIES

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Polynucleotide library used to determine cancerous states of mammalian
                                                   cancer cell line polynucleotide sequence SEQ ID NO:466.
                                                                                                                           breast cancer; oestrogen receptor-positive breast cancer; therapy; oestrogen receptor-negative breast cancer; lung cancer; ss.
                                                                                        colon cancer; tumour; diagnosis; gene expression product;
                                                                                                             detection; cancerous state; metastasis; identification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 291; 1097pp; English.
                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Williams LT, Escobedo
Reinhard C, Giese K,
Lamson G, Drmanac R,
Leshkowitz D, Kita D,
                                                                                                                                                                                                                                                                                                                                                                                                                                (CHIR ) CHIRON CORP. (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-126369/11.
                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                  WO9958675-A2
                  19-MAY-2000
                                                                                                                                                                                                                                                                                         13-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                          21-OCT-1998;
27-OCT-1998;
                                                                                                                                                                                                                                                                                                                          14-MAY-1998;
15-MAY-1998;
                                                       Human colon
                                                                                                                                                                                                                                                                                                                                                           15-MAY-1998;
                                                                                                                                                                                                                                                    18-NOV-1999
                                                                                          Human:
                                                                                                             probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cells
 The present invention describes isolated polynucleotides (PN) comprising a sequence selected from one of 835 nucleotide sequences given in AAA67073 to AAA67907. Heir (reverse) complements, sequences producing an Expectation (E) value of 0.01 or less compared to the 835 sequences, 835 sequences at least 50% identical to them, 200, 100, 40 or 20-mers of the 835 sequences that are degenerately equivalent or allelic to the 835 sequences. The polynucleotides are used to modify the activity of a polypeptide involved in a polysaccharide biosynthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pathway in the plant. They are especially used to modulate or alter the polysaccharide content, composition or structure of the plant. AAB16268 to AAB16340 are proteins encoded by some of the polynucleotide sequence
                                                                                                                                                                                                                                                                  Eucalyptus grandis; pinus radiata; Monterey pine; modification; plant cell wall; polysaccharide; polysaccharide biosynthetic pathway; transgenic plant; ds.
                                                                                                                                                                                                                                 Eucalyptus grandis alpha-glucosidase DNA sequence SEQ ID NO:197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New genes encoding proteins involved in a plant polysaccharide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    biosynthetic pathway, useful for modulating or altering the polysaccharide content, composition or structure of the plant
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Pred. No. 5.2e+02;
2; Mismatches 1; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GENE-) GENESIS RES & DEV CORP LTD.
(FLET-) FLETCHER CHALLENGE FORESTS LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 126; 301pp; English.
                                                                                                                      AAA67196 standard; DNA; 298 BP
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99US-0148426
                                                                                                                                                                                              (first entry)
                    184 ACTCCAAGGACTCCA 170
1 RCTCCANGGRCTCCA 15
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                                                                                                                                                                                                                                                                                                                                           Eucalyptus grandis.
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Best Local Similarity
Matches 12; Conserv
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                                                                                                                                                           AAA67196;
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ID AAA6
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Labat I;

J, Innis MA, Garcia PD, Sudduth-Kilinger of Randazzo F, Kennedy GC, Pot D, Kassam A; Crkvenjakov R, Dickson M, Dimanac S, Labb Garcia V, Jones LW, Stache-Crain B;

Escobedo J,

98US-0085426. 98US-0085537. 98US-0085696.

98US-0105234 98US-0105877

99WO-US10602

Sudduth-Klinger J;

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AAA00010 to AAA02716 represent polynucleotides isolated from CDNA libraries constructed from human colon cancer cell lines. The present libraries constructed from human colon cancer cell lines. The present denotine also describes a method of detecting differentially expressed genes correlated with a cancerous state of a mammalian cell, comprising detecting at least one differentially expressed gene product in a test sample derived from a cell suspected of being cancerous, where detection of the differentially expressed gene product is correlated with a cancerous state of the cell from which the test sample was derived. The polynucleotides sequences can be used in a method for detecting differentially expressed genes correlated with a cancerous state of a mammalian cell. The polynucleotides can also be used as probes for detecting and mapping related genes. They can be used in diagnosis and prognosis of disparent of the contraction of parameters of the contraction of the cell from the prognosic of the cell from the cell fro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pre-metastatic or metastatic cancerous states, stages of cancer, or responsivemess of cancer to therapy). This is particularly for breast cancer, oestrogen receptor-positive breast cancer, oestrogen receptor negative breast cancer, lung cancer, and colon cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Pred. No. 5.2e+02;
2; Mismatches 1;
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248 ACTCCACGGGCTCCA 234
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1 RCTCCANGGRCTCCA 15

δ qq AAA00475 standard; cDNA; 300 BP.

AAA00475, RESULT

AAA00475

polypeptide, chimeric proteins comprising Zcytor4 polypeptide and an affinity tag, and antibodies that specifically bind Zcytor4. Zcytor4 may play a role in intracellular adhesion and in the regulation or development of haematopoietic cells.

2222X8

Sequence 204 BP; 45 A; 45 C; 55 G; 51 T; 8 other;

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acute renal failure, acute nephritis, chronic renal failure, nephrotic syndrome, renal tubule defects, kidney transplants, toxic injury, hypoxic injury and trauma. The compounds are also useful for treating conditions such as neural degeneration where neural growth and regeneration are desirable, e.g., Alzheimer's disease, Parkinson's disease, Huntington's disease, Tourette's syndrome, amyotrophic lateral sclerosis, as well as motor neuron disease, demyelinating disease, bacterial diseases, viral diseases, and prion diseases including Greutzfeldt. Jakob disease. The compounds are also useful for treating disorders due to damage to neural tissue caused by neoplastic impingement, trauma or cerebrovascular events such as hemorrhage or emboli, and neural disorders such as mental retardation, autism, fetal alcohol syndrome, Down's syndrome and cerebral palsy. The present sequence represents an atisense oligo KD2-819 used in the characterisation of genomic clones for RetL5.
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                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This is the nucleotide sequence of an expressed sequence tag identified during the cloning of human cytokine receptor Zcytor4 cDNA (see AAV5596B). A cDNA containing 110 bp was obtained from human kidney cDNA library. The DNA was transfected into Escherichia coli strain DH10b and the plasmid was designated PSL690°. This has been used to generate probes to examine expression of Zcytor4. The invention provides Zcytor4 polynucleotides (see AAV5596B) and polynucleotides (see AAW80754-56), expression vectors, eukaryotic host cells which express Zcytor4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cytokine receptor; 2cytor4; human; cell proliferation; cell differentiation; cell adhesion; Burkitt's lymphoma; leukaemia; diagnosis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human cytokine receptor Zcytor4 expressed sequence tag.
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                                                                                                                                                                                                                                                                                                                                         Score 13.2; DB 22;
Pred. No. 5.1e+02;
                                                                                                                                                                                                                                                                                   Sequence 26 BP; 6 A; 8 C; 10 G; 2 T; 0 other;
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80.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAV55971 standard; DNA; 204
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Best Local Similarity 80.0
Matches 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1998-542279/46.
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Whitmore T;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                novel human cytokine receptors Ccytor4 cDNA. It was generated by PCR amplification (see AAV55972 and AAV55972) of a human foetal kidney CDNA library. The invention provides human and mouse cytokine receptor Ccytor4 polynuclectides (see AAV55968-69) and polypeptides (see AAW80754-57), expression vectors, eukaryotic host cells which express Ccytor4, chimeric proteins comprising a Ccytor4 polypeptide and an affinity tag, and antibodies that specifically bind Zcytor4. Zcytor4 may play a role in intracellular adhesion and in the regulation or development of haematopoietic cells.
                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human and mouse cytokine receptors, DNA and antibodies – also chimeric proteins, useful for promoting cell adhesion and diagnosing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This polynucleotide was generated as a probe for the isolation of
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   Length 204;
                                 Indels
                                                                                                                                                                                                                                                                                              Cytokine receptor; Zcytor4; human; cell proliferation; cell differentiation; cell adhesion; Burkitt's lymphoma; leukaemia; diagnosis; probe; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pownder TA;
Score 13.2; DB 19;
Pred. No. 5.2e+02;
2; Mismatches 1;
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                                                                                                                                                                                                                                                                   Human cytokine receptor Zcytor4 DNA probe.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            chimeric proteins, useful for pro
Burkitt's lymphoma and leukaemia
                                                                                                                                                                         BP.
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   88.0%;
80.0%;
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                                                                                                                                                                                                                                    (first entry)
Query Match 88.0
Best Local Similarity 80.0
Matches 12; Conservative
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                                                             1 RCTCCANGGRCTCCA 15
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57 ACTCCAAGGACTCCA 43
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Best Local Similarity
Matches 12; Conserv
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                                                                                                                                                                                                                                                                                                                                                             Synthetic.
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Example 1; Page 45; 176pp; Japanese.
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AAF57274
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                                                                                                                                                                            haemopoletin receptor protein family NR8 genes. The NR8 family sequences were initially searched for comparison on a nucleic acid database with the nucleic acid probe sequence TGGAGYNNNTGAGY encoding the amino acid sequence Trp-Ser-Xaa-Trp-Ser. The sequences AKS29238 ESS39300 and AAX290816-290925 represent specific examples of probe sequences used in the search. Antibodies to the NR8 family proteins are used for the diagnosis of blood formation disorders. Compounds identified
                                                                                                                                                                                                                                              as binding to the proteins are used for the treatment of such disorders.
                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                       Hemopoletin receptor protein family NR8 used for diagnosis of blood formation disorders -
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                                                                                                                                                                                                                                                                                           Length 15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Haemopoletin receptor family; NR8; antibody; diagnosis; blood formation disorder; fusion protein; probe; ss.
                                                                                                                                                                                                                                                                                            Score 13.2; DB 21;
Pred. No. 5.1e+02;
                                                               (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
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                                                                                                                                                                                                                                                               Sequence 15 BP; 2 A; 4 C; 6 G; 3 T; 0 other;
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                                                                                                                                                                                                                                                                                            88.0%;
80.0%;
                  99WO-JP03351
                                    98JP-0214720
98JP-0297409
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ID AAZ90922 standard; DNA; 15
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                                                                                                                                                                                                                                                                                                              12; Conservative
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15 GCTCCAAGGGCTCCA 1
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                                                                                   Maeda M;
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Best Local Similarity
Matches 12; Conserv
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                  23-JUN-1999;
                                    24 - JUN- 1998;
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29-DEC-1999
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The invention relates to the isolation of sequences encoding human haemopoietin receptor protein family NRB genes. The NRB family sequences were initially searched for comparison on a nucleic acid database with the nucleic acid probe sequence TGGAGYNNNTGGAGY encoding the amino acid sequence Trp-Ser-Xaa-Trp-Ser. The sequences ASIS9300 and AAIS90816-290925 represent specific examples of probe sequences used in the search. Antibodies to the NRB family proteins are used for the diagnosis of blood formation disorders. Compounds identified
                                                                                                                                                                                                                                                                                                                                                                                     as binding to the proteins are used for the treatment of such disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel Ret ligand polypeptide useful for suppressing growth of a tumor cell that expresses Ret and for modulating Ret signal transduction involving a cell expressing Ret polypeptide or Ret ligand polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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80.0%; Pred. No. 5.1e+02;
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Matches 12; Conservative
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15 GCTCCAGGGACTCCA 1
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AAZ90885/c
ID AAZ90885 standard; DNA; 15
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19-OCT-1998;
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                                              AAZ90885;
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used for the diagnosis of blood formation disorders. Compounds identified as binding to the proteins are used for the treatment of such disorders.
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80.0%; Pred. No. 5.1e+02;
                                                                                       Score 13.2; DB 21;
Pred. No. 5.1e+02;
2; Mismatches 1;
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                                             Sequence 15 BP; 2 A; 3 C; 6 G; 4 T; 0 other;
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                                                                                          88.0%;
80.0%;
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98JP-0297409
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                                                                                        Query Match 88.0
Best Local Similarity 80.0
Matches 12; Conservative
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15 ACTCCAGGGGCTCCA 1
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Best Local Similarity
Matches 12; Conserv
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19-OCT-1998;
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                                                                                                                                                                                                                                                                                     AAZ90863;
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ID AAZ908
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haemopoletin receptor protein family NR8 genes. The NR8 family sequences were initially searched for comparison on a nucleic acid database with the nucleic acid probe sequence TGGAGYNNNTGGAGY encoding the amino acid sequence Trp-Ser. The sequences AAZ59258-259300 and AAZ90816-280925 represent specific examples of probe sequences used in the search. Antibodies to the NR8 family proteins are used for the diagnosis of blood formation disorders. Compounds identified as binding to the proteins are used for the treatment of such disorders.
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                                              Haemopoietin receptor family; NR8; antibody; diagnosis; blood formation disorder; fusion protein; probe; ss.
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Pred. No. 5.1e+02;
2; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                             (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 1; Page 43; 176pp; Japanese.
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80.0%;
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98JP-0297409
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Human NR8 gene probe #113.
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Best Local Similarity 80.0
Matches 12; Conservative
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The invention relates to the isolation of sequences encoding human haemopoietin receptor protein family NRB genes. The NRB family sequences were initially searched for comparison on a nucleic acid database with the nucleic acid probe sequence TGGAGYNNNTGAGY encoding the amino acid sequence Trp-Ser-Xaa-Trp-Ser. The sequences AAX59258-559300 and AAX90816-290925 represent specific examples of probe sequences used in the search. Antibodies to the NRB family proteins are used for the diagnosis of blood formation disorders. Compounds identified
                                                                                                                                                                                                                                                                                                                                                           as binding to the proteins are used for the treatment of such disorders.
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                                                                                    Hemopoletin receptor protein family NR8 used for diagnosis of blood
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                                                                                                                                            Example 1; Page 41; 176pp; Japanese.
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98JP-0297409
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15 GCTCCAGGGACTCCA 1
                                           WPI; 2000-116933/10.
                                                                                                         formation disorders
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    Nomura H, Maeda M;
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19-OCT-1998;
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Haemopoietin receptor family; NR8; antibody; diagnosis;
blood formation disorder; fusion protein; probe; ss.
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Pred. No. 5.1e+02;
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ID AAZ90850 standard; DNA; 15 BP.
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80.0%;
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98JP-0297409
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15 GCTCCAGGGACTCCA 1
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Best Local Similarity
                                                              Homo sapiens.
                                                                                                   WO9967290-A1
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Haemopoietin receptor family; NR8; antibody; diagnosis; blood formation disorder; fusion protein; probe; ss.
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                      1 RCTCCANGGRCTCCA 15
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15 ACTCCATGGACTCCA'1
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ID AAZ908
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                                                                                                                                                                                                                                                                               Gaps
                                  5 Degenerate hybridisation probes (AAT17870-74) are based on a conserved motif (AAR92812) found in haemopoietin receptors. The probes are used in the identification and/or cloning of genes coding for novel haemopoietin receptors, e.g. the murine interleukin-11 (IL-11) receptor alpha chain gene (AAT17868) receptors are defined by their ability to hybridise to the probes under medium stringency conditions.
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                                                                                                                                                                                                                                                                         0; Mismatches
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Claim 12; Page 52; 87pp; English.
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Matches 15; Conservative
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                                                Hemopoietin receptor protein family NR8 used for diagnosis of blood formation disorders - \,
                                                                                                                                                                                          The invention relates to the isolation of sequences encoding human
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Best Local Similarity 80.0
Matches 12; Conservative
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WPI; 2000-116933/10
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88.0%; Score 13.2; DB 21; Length 15; 80.0%; Pred. No. 5.1e+02; 1ive 2; Mismatches 1; Indels (

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Query Match Best Local Similarity Matches 12; Conserv

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August 29, 2001, 20:16:43; Search time 301.32 Seconds (without alignments) 31.258 Million cell updates/sec
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/SIDS8/gcgdata/geneseq/geneseqn/Na2000_DAT:*
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                OM nucleic - nucleic search, using sw model
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

UMMARIES
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Result		Query				
No.	Score	Match	re Match Length DB I	DB	ID	Description
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-	13.2	88.0	15	17	AAT17873	Haemopoietin recep
o 0	13.2	88.0	15	21	AAZ59273	Human NR8 gene pro
°	13.2	88.0	15	21	AAZ90833	Human NR8 gene pro
O 4	13.2	88.0	15	21	AAZ90834	Human NR8 gene pro
c S	13.2	88.0	15	21	AA290850	Human NR8 gene pro
9 0	13.2	88.0	15	21	AA290853	Human NR8 gene pro
c 7	13.2	88.0	15	21	AA290863	Human NR8 gene pro
۵ د	13.2	88.0	15	7	AAZ90885	Human NR8 gene pro
σ 0	13.2	88.0	15	21	AAZ90890	Human NR8 gene pro
c 10	13.2	88.0	15	21	AA290922	Human NR8 gene pro
11	13.2	88.0	56	22	AAF57274	Antisense oligo KD

Human cytokine rec	cytokine	Eucalyptus grandis	Human colon cancer	G-CSF receptor lig		Squirrel Monkey co	SOMCIP full-length	Ly-6 terminal CIP	Mouse G-CSF recept	Human colon cancer	DNA encoding cytok		Murine EST AU03593		Human TANGO 204 po		Mouse RetL5 polype	DNA encoding cytok	Murine glial deriv	Gene for AHSV. Af	Mouse TANGO 204 po	Mouse TANGO 204 va	Mouse TANGO 204 va	Mouse TANGO 204 va	DNA sequence encod	DNA sequence encod	Human prostate can	Human interleukin-		Human ORFX ORF2727	Nucleotide sequenc	Nucleotide sequenc	Nucleotide sequenc
AAV55971	AAV55980	AAA67196	AAA00475	AAT33517	AAZ42586	AAQ84638	AAQ99109	AAT03334	AAT33515	AAA02109	AAT35141	AAF57273	AAF31057	AAF57271	AAC84378	AAC84386	AAF57270	AAT35137	AAZ28259	AAQ30130	AAC84385	AAC84396	AAC84397	AAC84398	AAV63614	AAV63541	AAF15587	AAV02978	AAF21936	AAC77172	AAZ00367	AAZ00343	AAZ00379
19	13	21	21	17	21	16	16	16	17	21	17	22	22	22	22	22	22	17	20	13	22	22	22	22	19	19	21	19	21	21	20	20	20
204	211	298	300	324	349	396	396	396	639	725	765	783	792	795	795	795	834	1002	1019	1178	1293	1293	1293	1293	1590	1590	1607	1656	1874	97	6	2087	2166
88.0	88.0	88.0	88.0	88.0	88.0	88.0	88.0	88.0	88.0	88.0	88.0	88.0	88.0	88.0	88.0	88.0	88.0	88.0	88.0	88.0	88.0	88.0	88.0	88.0	88.0	88.0	88.0	æ	ω	ω.	88.0	88.0	88.0
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ALIGNMENTS

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Haemopoietin; interleukin-11; IL-11; receptor; agonist; antagonist; therapy; diagnosis; probe; hybridisation; ss.
                                                                                                                                                                                                                                                                                                      Nucleic acid encoding haemopoietin receptor containing conserved amino acid motif esp. IL-11 receptor alpha chain - used for developing IL-11 (ant)agonists
                                                                              Haemopoietin receptor probe HYB4.
                                                                                                                                                                                                                                           (AMRA-) AMRAD OPERATIONS PTY LTD.
                 AAT17873 standard; DNA; 15 BP.
                                                                                                                                                                                           95WO-AU00578.
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94AU-0007901
                                                          (first entry)
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05-SEP-1994;
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                                                                                                                              Synthetic.
                                      AAT17873;
RESULT
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D45552 235 bp mRNA EST 20-FEB-1995
HUMGS02739 Human adult lung 3' directed MboI cDNA Homo sapiens cDNA
3', mRNA sequence.
D45552 GI:662506
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 235)

Itoh,K., Okubo,K., Yosii,J., Yokouchi,H. and Matsubara,K.

DNA expression profile of active genes in human lung

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Human adult lung 3' directed MboI cDNA"
/note="Adult human lung, 3' directed MboI"
a 85 c 55 g 48 t 6 others
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 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Kohichi Itoh
Institute for Molecular and Cellular Biology
Osaka University
3-1, Yamadaoka, Sulta, Osaka, 565, Japan
Tel: 06-877-5111 x3910
Fax: 06-877-1922.
 Mismatches
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Matches 12; Conservative
Conservative
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66 GCTCCAGGGACTCCA 52
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Search completed: August 29, 2001, 19:22:17 Job time: 24140 sec us-09-532-263-9.rst

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Matches 12; Conserv
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AA587324/C
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EST231419 Normalized rat ovary, Bento Soares Rattus sp. cDNA clone
ROVCI69 3' end, mRNA sequence.
                                                                                                        /clone_lib="RIKEN full-length enriched, 11 days pregnant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryotà; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 232)
Lee.N.H., Glodek,A., Chandra,I., Mason,T.M., Quackenbush,J.,
Kerlavage,A.R. and Adams,M.D.
Rat Genome Project: Generation of a Rat EST (REST) Catalog & Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
visit our web site (http://genome.rtc.riken.go.jp)
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Pred. No. 5.5e+03;
2; Mismatches 1; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gene Index
Unpublished (1998)
Contact: Lee, NH
The Institute for Genomic Research
9712, Medical Center Drive, Rockville, MD 20850, USA
Tel: (301) 838-3529
Fax: (301) 838-3208
Email: nhlee@tigr.org
Seq primer: M13-21.
                                                                                                                      adult female ovary and uterus"
                                                                                                                                                                                                                                                                                                                                                                                                                                  61 t
                                                    /organism="Mus musculus"
                                                                               /db_xref="taxon:10090"
                          Location/Qualifiers
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                                                                                             /clone="5033406C17
                                                                 /strain="C57BL/6J
                                                                                                                                  /sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AI234857.1 GI:3828363
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80.0%;
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Best Local Similarity 80.0°
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92 ACTCCATGGACTCCA 106
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/note="Organ: colon; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from RER+ colon tumor, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is not normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo (Soares4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cDNA Library Preparation: M. Bento Soares, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NGI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 54 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 153.

Location/Qualifiers
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Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Issue Procurement: Ilan Kirsch, M.D., Michael R. Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA587324 233 bp mRNA EST 26-SEP-1997 nn78e01.s1 NCI_CGAP_CO9 Homo sapiens cDNA clone IMAGE:1090008 3',
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                /clone_lib="Normalized rat ovary, Bento Soares"
/hote="Organ: ovary; Vector: pT/T3Pac; Site_1: EcoRI;
Site_2: NotI"
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/db_xref="taxon:9606"
/clone="IxAGE:1090008"
/tlssue=Iype="rolor CGAP_CO9"
/tlssue=rype="color tumor RER+"
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                                                                                                                                                                                                                                                                                                                        Score 13.2; DB 17;
Pred. No. 5.5e+03;
/organism="Rattus sp."
/db_xref="ATCC (inhost):2040521"
/db_xref="taxon:10118"
/clone="ROVCI69"
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216 GCTCCAGGGACTCCA 202
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Best Local Similarity
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Gaps

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I (Dases 1 to 230)

E (Mono, H., Aizawa, K., Akahira, S., Akiyama, J., Carninci, P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Hori, F., Ishikawa, T., Itoh, M., Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N., Kojima, Y., Roya, S., Kusakabe, M., Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y., Owa, C., Ozawa, Y., Saito, H., Sano, M., Sato, K., Shibata, Y., Shibata, Y., Shibata, Y., Shibata, Y., Shibata, Y., Shibata, Y., Sauti, H., Takahashi, F., Tateno, M., Tominaga, N., Tsunoda, Y., Yoshino, M., Muramatsu, M. and Hayashizaki, Y. RIKEN Mouse ESTS (Konno, H., et al. 1999)
                   Transcriptional sequencing: A method for DNA sequencing using RNA polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998) Itoh, M., Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J., Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y. Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
Carninci, P. and Hayashizaki, Y. High-efficiency full-length cDnA cloning. Methods Enzymol. 303, 19-44 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AV288298 230 bp mRNA EST 09-NOV-1999 AV288298 RIKEN full-length enriched, 11 days pregnant adult female ovary and uterus Mus musculus cDNA clone 5033406C17, mRNA sequence.
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URL:http://genome-rtc.riken.go.jp,
Saski,N., Izawa,M., watahiki,M., Ozawa,K., Tanaka,T., Yoneda,Y.,
Matsuura,S., Carninci,P., Muramatsu,M., Okazaki,Y. and Hayashizaki
Division of Experimental Animal Research in Riken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The Institute of Physical and Chemical Research (RIKEN), Genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Yoshihide Hayashizaki
Genome Exploration Research Group, Life Science Tsukuba Center,
Genome Science Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
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3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: +81-228-36-9013
Fax: +81-298-36-9098
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29 ACTCCAAGGACTCCA 15
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bassa 1 to 27)
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1 Enkuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Hori, F., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Hori, F., Ishi, Kawai, J., Itoh, M., Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N., Kojima, Y., Koya S., Kusakabe, M., Okazaki, Y., Owa, C., Ozawa, Y., Saito, H., Sano, M., Sato, K., Shibata, Y., Shigemoto, Y., Shiraki, T., Soqabe, Y., Suqahara, Y., Suzuki, H., Suzuki, H., Yakinaga, N., Tsunoda, Y., Watahiki, A., Watanabe, S., Yamamura, T., Yasunishi, A., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.

I Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Transcriptional sequencing: A method for DNA sequencing using RNA polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998) Itch, M., Kitsunai, T., Akiyama, J., Ibbata, K., Izawa, M., Kawai, J., Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramateu, M., Okazaki
                                                                                                                                                                                                                                 AV282369 227 bp mRNA EST 08-NOV-1999
AV282369 RIKEN full-length enriched, adult male testis (DH10B) Mus musculus cDNA clone 4933429K08 3' similar to AB029026 Homo sapiens MV282369. GISARA1103 protein, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: +81-298-36-9013
Fax: +81-298-36-9098
Email: genome-resettc.riken.go.jp,
URL:http://genome.rtc.riken.go.jp/
Sasaki,N., Izawa,M., Watahiki,M., Ozawa,K., Tanaka,T., Yoneda,Y.,
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Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 465-470 (1999)
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Yoshihide Hayashizaki
Genome Exploration Research Group, Life Science Tsukuba Center,
Genome Science Laboratory
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/dev_stage="adult"
/lab_host="alult"
/lab_host="Site_1: SalI; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Please visit our web site (http://genome.rtc.riken.go.jp) for
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="4933429K08"
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                   1 RCTCCANGGRCTCCA 15
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205 ACTCCATGGCCTCCA 191
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REFERENCE AUTHORS us-09-532-263-9.rst

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BACKWARD: ATTAACCTCACTAAAG
Insert Length: 226 Std Error: 0.00
Plate: BP330010A20 row: B column: 6
Seq primer: AGCGGATAACAATTTCACACAGGA
High quality sequence stop: 226.
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low stringency conditions.
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/clone="BP230010A20B6"
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80.0%;
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Best Local Similarity 80.0°
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Unpublished (2000)
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Best Local Similarity 80.0 Matches 12; Conservative
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200 GCTCCATGGACTCCA 214
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"Organism="Homo sapiens"

"Ab_rate="taxon:9606"

"Clone_lib="UT0047"

"Adv. stage="Adult"

"Ancte="Corgan: uterus_tumor; Vector: pucl8; Site_l: Smal;

Site_2: Smal; A mini-library was made by cloning products

Gerived from ORESTES POR (U.S. Letters Patent application

No. 196, 716 - Ludwig Institute for Cancer Research)

Profiles into the pUC 18 vector. Reverse transcription of

tissue mRNA and cDNA amplification were performed under
             Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1 (bases 1 to 221)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Magai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare Simpson, A.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
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Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=MR0&t2=MR0-UT0047-
080900-201-d07&t3=2000-09-08&t4=1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BF380015 221 bp mRNA EST 27-NOV-2000
MRO-UT0047-080900-201-d07 UT0047 Homo sapiens CDNA, mRNA sequence.
BF380015
GAGAGAGAGGATCCAAGAGCTCTTTTTTTTTTTTVN 3'], cDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Simpson A.J.G.
Laboratory of Gancer Genetics
Ludwig Institute for Cancer Research
Fua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Shorgun sequencing of the human transcriptome with ORF expressed
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Pred. No. 5.4e+03;
2; Mismatches 1;
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Fax: 217 244 5617
Email: h-lawineiuc.edu
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Email: h-lawineiuc.edu
Research Initiative, Animal Genome Resource Grant AG 99-3205-8534
to H. A. Lewin and J. E. Womack. Base Calling/Quality Scores: PHRED
from Washington University Genome Center. Vector Trimmi 9:
Cross_match from Washington University Genome Center PHRAP suite.
Sequences submitted are vector free and at least 200 bp in length.
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1 (bases 1 to 226)
Lewin,H.A., Soares,M.B., Rebeiz,M., Pardinas,J., Liu,L. and Larson
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/lab_host="Duff"
/lab_host="Duff"
/lab_host="Organ: placenta; Vector: pT7T3Pac; Site_1: EcoRI;
Site_2: NotI; The cDNA library was contributed by the
Soares laboratory and it was constructed and normalized
as described by Bonaldo, M.F., Lennon, G. and Soares,
M.B. (1996), Genome Research 6(9): 791-806. "
3 49 c 60 g 65 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Lewin, H. A. W. M. Keck Center for Comparative and Functional Genomics W. M. Keck Center for Comparative and Functional Genomics of Illinois at Urbana-Champaign 340 Edward R. Madigan Laboratory, 1201 W. Gregory Dr., Urbana, IL 61801, USA
                                                                                                                                                                                                                                                                                                                                                                      AW462741 226 bp mRNA EST 24-FEB-2000 BP230010A20B6 Soares normalized bovine placenta Bos taurus cDNA clone BP230010A20B6 5', mRNA sequence. AW463741 GI:7032909
                                                                           Gaps
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Score 13.2; DB 148; Length 221;
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Pred. No. 5.5e+03;
2; Mismatches 1; Indels 0;
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153 GCTCCATGGGCTCCA 167
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Marrah., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Gelsel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Thelsing, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
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                                                                                                                                                                                                                                                                                                                 ms24a10.rl Stratagene mouse skin (#937313) Mus musculus cDNA clone IMAGE:607866 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
mRNA and cDNA amplification were performed under low stringency conditions." $46\ c\ 49\ g\ 48\ t
                                                                                                                                            Gaps
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Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                      Score 13.2; DB 120; Length 198;
Pred. No. 5.4e+03;
2; Mismatches 1; Indels 0;
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/clone_lib="Stratagene mouse skin (#937313)"
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Location/Qualifiers
1. .199
/organism="Mus musculus"
/strain="C57BL/6"
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The WashU-HHMI Mouse EST Project
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1 RCTCCANGGRCTCCA 15

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Transcriptional sequencing: A method for DNA sequencing using RNA polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998) Itoh, M., Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J., Tomaru, Y., Carninci, P., Shibata, Y., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y. Automated filtration based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
Carninci, P. and Hayashizaki, Y. High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
AV340647 202 bp mRNA EST . 11-NOV-1999
V34340647 RIKEN full-length enriched, adult male olfactory bulb Mus
musculus cDNA clone 6430516D09 3', mRNA sequence.
AV340647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: +81-298-36-9013
Fax: +81-298-36-9098
Email: genome-resettc.riken.go.jp,
URL:http://genome.rtc.riken.go.jp/
Sasaki,N., Izawa,M., Watahiki,M., Ozawa,K., Tanaka,T., Yoneda,Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Site_1: Sall; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project to Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKBN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The Institute of Physical and Chemical Research (RIKEN), Genomic
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Concome Exploration Research Group, Life Science Tsukuba Center,
Genome Science Laboratory
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Please visit our web site (http://genome.rtc.riken.go.jp) for
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/db_xref="taxon:10090"
/clone="6430516D09"
/clone="lb="RIKEN full-length enriched; adult male olfactory bulb"
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/dev_stage="adult"
/lab_host="DH10B"
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Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Parayed by: Greg Lennon, Ph.D.
CDNA Library Parayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrpy/image/image.html
Insert Length: 1894
Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 133.
                                                                                                                                                                                                                                                                 Tel: 81-298-36-9145
Fax: 81-298-36-9145
Fax: 81-298-36-909
Fax: 81-298-36-909
Email: genome-resertc.riken.go.jp
Thermostabilization and thermoactivation of thermolabile enzymes by
trehablose and its application for the synthesis of full length cDNA
(Proc. Natl. Acad. Sci. U.S. A. 95(2):520-524 (1998))
Transcriptional sequencing: A method for DNA sequencing using RNA
polymerase (Proc. Natl. Acad. Sci. U.S. A. 95(7):3455-3460 (1998))
Please visit our web site (http://genome.rtc.riken.go.jp) for
further details.
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Kikuchi, N., Kojima, Y., Matsuyama, T., Niitsuma, H., Oda, H., Owa, C., Sato, K., Shibata, Y., Shigemoto, Y., Shiraki, T., Sogabe, Y., Sugahara, Y., Suzuki, H., Szuki, H., Tateno, M., Tomaru, Y., Tominaga, N., Watanabe, S., Yagame, M., Yamamura, T., Yokota, T., Yoshino, M., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y.
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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/db_xref="taxon:10090"
/clone="2510207N04"
/clone=11b="Mus musculus C57BL/6J 10-day embryo"
/sex="mixed"
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Pred. No. 5.4e+03;
2; Mismatches 1; Indels 0,
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A1933508
A1933508.1 GI:5672245
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80.0%;
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Best Local Similarity 80.0
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                                                                                                                                                                          Contact: Chie Owa
                                                                                                                          RIKEN Mouse ESTs
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Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Seq primer: puc 18 forward forward High quality sequence stop: 198.
Location/Qualifiers
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//dev_stage="Adult"
//note="Organ: uterus; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196 ,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: Sall; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.85 kb. Life Technologies catalog #: 11539-012"
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0V4-UM0094-280300-152-a01 UM0094 Homo saplens CDNA, mRNA sequence.
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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/tlssue_type="moderately-differentiated endometrial adenocarcinoma, 3 pooled tumors"
/lab_host="DH10B"
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Pred. No. 5.4e+03;
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                                                                                                          /organisma"Homo sapiens"
/db_xref="taxon:9606"
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/db_xref="taxon:9606"
/clone_lib="UM0094"
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Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
Location/Qualifiers
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Best Local Similarity 80.0
Matches 12; Conservative
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Carninci, P., Nishiyama, Y., Westover, A., Itoh, M., Nagaoka, S., Sasaki, N., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S. A. 95 (2), 520-524 (1998)
Itoh, M., Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J., Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y.
Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 182)
Carninci, P., Shibata, K., Ozawa, Y., Konno, H., Itoh, M., Aizawa, K.,
Akahira, S., Akiyama, J., Fukuda, S., Fukunishi, Y., Funayama, T., Hara, A., Hayatsu, N., Hori, F., Ishikawa, T., Itoh, M., Izawa, M., Kawai, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Site_1: Sall; Site_2: BamHI: cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  primed with a primer [5' GAGAGAGAAGGATCCAAGAGGTTTTTTTTTTTTTTVN 3'], cDNA was
                                                                                                                                                                                                                                                     Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA-cloning. Methods Enzymol. 303,
19-44 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="B430304H06"
/clone_lib="RIKEN full-length enriched, 4 days neonate
                                                                                                                                                                                                                                                                                                                                           Please visit our web site (http://genome.rtc.riken.go.jp) for further details.
Location/Qualifiers
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AV118281 Mus musculus C57BL/6J 10-day embryo Mus musculus CDNA
Clone 2610207N04, mRNA sequence.
AV118281
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Pred. No. 5.4e+03;
2; Mismatches 1; Indels 0;
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/dev_stage="4 days neonate"
/lab_host="DH10B"
JRL:http://genome.rtc.riken.go.jp/
                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Mus musculus"/db_xref="taxon:10090"
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80.0%;
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58 GCTCCAGGGGCTCCA 44
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (basea 1 to 170)
S Aizawa,K., Akahira,S., Akimura,T., Arai,A., Arakawa,T., Carninci,P., Hanagaki,T., Hayatsu,N., Hiraoka,T., Hirozane,T., Hodoyama,Y., Imotani,K., Ishi,Y., Itoh,M., Izawa,M., Kawai,J., Kojima,Y., Konno,H., Kusakabe,M., Matsuyama,T., Miyazaki,A., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Okido,T., Okido,T., Owa,C., Sakai,C., Sakai,C., Sakai,C., Sakai,C., Sakai,C., Sakai,C., Sakai,C., Shibata,X., Shibata,X., Shinagawa,A., Shiraki,T., Soapbe,Y., Suzuki,H., Tagwaw,A., Takahashi,F., Tanaka,T., Toya,T., Watahiki,A., Wamamura,T., Yasunishi,A., Yoshiki,A., Muramatsu,M. and Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                         CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 632 Std Error: 0.00
Seq primer: -400P from Gibco
High quality sequence stop: 107.
Location/Qualifiers
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The Institute of Physical and Chemical Research (RIKEN), Genomic
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cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
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Tel: +81-298-36-9013
Fax: +81-298-36-9098
Email: genome-res@ttc.riken.go.jp,
                                                                                                                                                                                                                                                                                                                                           /clone="IMAGE:2011202"
/clone_lib="NCI_CGAP_Brn23"
/tissue_type="q1ioblastoma (pooled)"
/lab_host="DH10B"
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Pred. No. 5.3e+03;
2; Mismatches 1;
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/organism="Homo sapiens"
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Contact: Yoshihide Hayashizaki
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Description	AA644792 vs82d07.r A1371456 qy06c02.x BB593914 BB593914	AV118281 AV118281 A193508 WANT 4 606.x	AW004039 V44 - 0M003 AA163051 ms24a10.r AV340647 AV340647	BF38015 MF462741 BP230010A	AV282369 AV288298 AV288298	A1234857 EST231419 AA587324 nn78e01.s	D45552 HUMGS02739 AA089075 mc63a01.r	T0328 1B123 Inta C1257 C1257 Yuji H32365 EST107377 R	ALIBS438 qes3d09.x BB180104 BB180104 F37625 HSPD05393 H	AA653297 ag65c06.s F01487 HSC04D122 n	AA34030 EST40241 BF714533 mab01e01. BB313512 BB313512	AI547450 UI-R-C3-S AA494436 ne28d04.S	AI606963 vw36f02.x BF228467 BP250008B	BB461437 BB461437 BE631643 uu63a05.y	AA288582 mp15905.r BF714534 mab01e01.	BF290833 EST455424 AZ227737 RPC1-23-8 H34301 EST111113 R	F21363 HSPD05876 H RF36338 CM2-NN011	BF010839 NXI NXI AA963063 111-P-F1-F	BF931642 IL2-NT020 AA822320 vw36f02.r AI465630 vw36f02.v		AA644792 100 bp mRNA EST 28-OCT-1997 V\$82d07.r1 Barstead mouse myotubes MPLRB5 Mus musculus cDNA clone MAGE:1122781 5' similar to gb:M80359 PUTATIVE SERINE/THREONINE-PROTEIN KINASE P78 (HUMAN); gb:X70764 M.musculus	Kinase (MOUSE);, mRNA sequence. ,	Craniata; Vertebrata; Euteleostomi;	Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Lacy,M., Le,M., Martin,J., Morris,M.,
SUMMARIES. Query Match Length DB ID		182 25	199 3	221 14	227 28	232 17	235 15		250 12 250 12 251 15	253 10 255 15	260 16 260 16 262 13	264 21 268 8	271 22 271 14	275 13 275 13	276 4 276 16		286 15	288	88.0 295 171 BF931642 88.0 296 12 AB82320 88.0 296 20 AI465630		92 100 bp mRNA 7.r1 Barstead mouse myotubes 1152781 5. similar to 9b:480 7THREONINE-PROTEIN KINASE P7	or serine/threonine protein 92 92.1 GI:2571221	s Metazoa; Chordata;	l to 100) Hillier,L., Allen,M Kucaba,T., Lacy,M.,
% Result Qu No. Score Ma	13.2	5 13.2	13.2	9 13.2 10 13.2	13.2	13.2	15 13.2 16 13.2	13.2	13.2	23 13.2	13.2	28 13.2 29 13.2	30 13.2 31 13.2	32 13.2 33 13.2	13.2	13.2	39 13.2	13.2	43 13.2 44 13.2 13.2		RESULT 1 AA644792 LOCUS AA644792 DEFINITION vs82d07. IMAGE:11.	MKNA IOT SE ACCESSION AA644792 VERSION AA644792.1 KEYWORDS EST.	Σ	REFERENCE 1 (bases AUTHORS Marra,M., Geisel,S.,

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qy06c02.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2011202 3',
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1 (bases 1 to 151)
NOILYNINDS-CAGAP HITLE;//www.ncbi.nlm.nih.gov/ncicgap.
NOILYNINDS-CAGAP HITLE;//www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAPAFBTGAP); Tumor Gene Index
(Unpublished (1998)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Pissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D., Ph.D.
                                                                                                                                                            Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU HHMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty.free through LLNL; contact the
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Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B. Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.
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Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 1.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

em_esthum13:*
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
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em_estpl8:*
em_estpl9:*
em_estpl10:*

em_estpl5: em_estpl6:

em_estp14

em_estro19: em_estro20: gb_est25:*

gb_est26: gb_est27: gb_est28: gb_est29:

gb_est30: gb_est31: gb_est32:

gb_est41: gb_est42: gb_est43: gb_est44: gb_est44:

gb_est46: gb_est47:

em_estrog:*
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em_estrol1:*
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em_estrol5:*
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em_estrol7:*
em_estrol8:*

em_estro8:*

em_estrol: em_estro2: em_estro3: em_estro4: em_estro5: em_estro5:

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Psyssinkiirtwoopphupldyrclspehtlibesavpesposdsggsysing
LLGITQTTAOGKReHDDSODESCHSVDSQGSGGGRRKOLRTEHFPSAALDGGFERHY
SSDSFSQSKAEQQLYPLALMNPGLDEGKGASSISRNLAAHQGYAVVTEALQPLPLCLK
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Direct Submission
Submitted (19-JUN-1998) Institute of Molecular Pathology, Dr.
Bohr-Gasse 7, Vienna A-1030, Austria
Location/Qualifiers
1. 1290
/organism="Danio rerio"
/db_xref="taxon:7955"
<1. .1290
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/rpt_family="Alu-Jo"
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a 280 c 329 g
293. .323
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SSYSEAWRRTNSSILGSPYYYSFANRPPPAGAFDHL"
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AND ACCCAYTTRCTCCA 472

Search completed: August 29, 2001, 19:52:03

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                                                                                                                                               Direct Submission
Submitted (12-MAY-1998) Biochemistry, Univ. of Texas Health Science
Center at San Antonio, 7703 Floyd Curl Dr., San Antonio, TX 78284,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ó
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Direct Submission
Submitted (04-DEC-1992) to the DDBJ/EMBL/GenBank databases.
Tadetsugu Taniguchi, Osaka University, Institute for Mol. and Cell.
Biology: Suite-shi, Osaka 565, Japan (Tel:06-877-5289, Fax:06-878-9846)
                                                                Members of the Mouse retrovirus-related repetitive sequence MuERVC recovered from C57BL/6J and SPRET/Ei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (strain:C57BL16) spleen cDNA to mRNA, clone_lib:mouse spleen cell cDNA.
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 1063)
Hardies,S.C.
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/note="similar to the gag-pol of Moloney Murine Leukemia
virus"
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
1 (bases 1 to 1165)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IL-2 receptor; cytokine receptor family; gammachain; mouse IL-2R
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Pred. No. 1.8e+03;
3; Mismatches 0; Indels 0;
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Mouse mRNA for mouse IL-2R gamma, complete cds.
D13821
                                                                                                                                                                                                           Location/Qualifiers
1. 1063
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Tadatsugu Taniguchi
Institute for Molecular and
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Cellular Biology, Osaka University
                                                                                                                                                                                                                                                                                                                                                                  /rpt_type=dispersed
/rpt_family="MuERVC"
196 c 297 g
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Location/Qualifiers
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80.0%;
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Hardies, S.C.
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RYTFRVRSRYNPICGSSQQWSKWSQPVHWGSHTVEENPSLFALEAVLIPVGTWGLIIT
LIPPKGALGEGFGGSPGSLHSPYWPPPCYSLKPEA"
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Homo sapiens partial IL-12RB1 gene for IL-12 receptor betal chain,
exons 6-7.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                  /clone_lib="mouse spleen cell cDNA"
/tissue_type="spleen"
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Elloumi-Zghal, H., Abdelhak, S. and Dellagi, K.
Genomic structure of IL12RB1 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 13.8; DB 94;
Pred. No. 1.8e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AJ297692
AJ297692.1 GI:10443211
IL-12 receptor betal chain; IL-12RB1 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="mouse IL-2R gamma" 74. .1114
/gene="mouse IL-2R gamma" 74. .7/product="mouse IL-2R gamma" 292 c 276 g 289 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Mismatches
                                                                                                                                                                                             /gene="mouse IL-2R gamma"
                                                                                                                                             /gene="mouse IL-2R gamma'
8. .1117
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/db_xref="taxon:9606"
                                           /db_xref="taxon:10090"
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/rpt_family="Alu-Jb"
/rpt_type=DISPERSED
1. .1187
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                                                                                                                                                                                                                         /codon_start=1
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Best Local Similarity 80.0
Matches 12; Conservative
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733 GCTCCATTTACTCCA 719
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KGFYEPNIESAINDVHNFSIKDVGTIITNKTGVSPEGVSQTDYWAFSGTVTDDSLPPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPITVLVFGLPVSATTGMTAIEFVAKVRVALQEAIASFTAINSYKDHPTDGSKLEVTY
LDNQKHVLSTYSTYGITISQEIISESKPGYGTWNLLGAQTVTLDNQQTPTVFYHFERT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="MSNNTYQHVSNESRYVKFDPTDTNFPPEITDVQAAIAAISPAGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="c in wild type; t in amber mutants N128, NG115 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      western European house mouse.
Mus musculus domesticus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                  Viruses; dsDNA viruses, no RNA stage; Tailed phages; Myoviridae;
T4-like phages.
                                                                    Tition projects to 1034)

Barrett, B.K. and Berget, P.B.
Laboratory methods using transposon Tn5 insertions to sequence bacteriophage T4 gene 11

DNA 8, 287-295 (1989)

89356257

Braft entry and computer readable copy of sequence [1] kindly provided by P.B.Berget, 20-JUL-1989.

The reading frame for gpl2 is in disagreement with Selivanov et al., (Accession #X06792).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note="c in wild type; t in amber mutants N108 and N93"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              207. .866
/note="baseplate structural protein (gpl1)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 13.8; DB 11;
Pred. No. 1.8e+03;
Bacteriophage T4 DNA, clone pJZ1 and pBB1.
                                                                                                                                                                                                                                                                                                        /organism="Bacteriophage T4"
/db_xref="taxon:10665"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /trans1_table=11
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/db_xref="GI:215858"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         863. .>1034
/note="gp12 protein"
                                                                                                                                                                                                                                                                                                                                                                       /note="gpl0 protein"
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80.0%;
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1002 ACTCCATTTACTCCA 988
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                  Bacteriophage T4
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Matches 12; Conserv
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AF064721/c
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RITWLFSSGYDDFTLLKTTGDLPKEESFFFMCHKTLFPTSFDITTDFT
KIKGGLQEVAADQLDYKRQGRRHQAGSDALLTAATFFKIKKQFFGDNWNQIAPLICGHM
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Draper.M.P., Salvadore,C. and Denis,C.L.
Identification of a mouse protein whose homolog in Saccharomyces cerevisiae is a component of the CCR4 transcriptional regulatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (28-FEB-1995) Christopher Salvadore, Biochemistry
Department, University of New Hampshire, Main Syreet, Durham, NH
03824, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PT4G11A 1034 bp DNA PHG 28-APR-1993
Bacteriophage T4D gene 11 encoding baseplate structural protein (gp11) complete cds, gene 10, 3' end, and gene 12, 5' end. M26253
M26253 I G1:215856
baseplate structural protein; gp10 gene; gp11 gene; gp12 gene.
                                                                                                Gaps
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Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis
                                                          Length 979;
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240 c 240 q 269 t
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Pred. No. 1.8e+03;
3; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mol. Cell. Biol. 15 (7), 3487-3495 (1995)
95311945
                                                      Score 13.8; DB 14
Pred. No. 1.8e+03;
                                                                                            Mismatches
                                                                                                                                                                                                                                                                                          Caenorhabditis elegans cCAF1
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80.0%;
                                                      92.0%;
80.0%;
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Salvadore, C.
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Best Local Similarity 80.0
Matches 12; Conservative
                                                                                              Conservative
                                                                                                                                                       :|||||:||:||||
425 ACTCCATTTACTCCA 439
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                                                                                                                                   1 RCTCCAYTTRCTCCA 15
                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                      CEU21854
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Anopheles gambiae STS SP6 end of clone 02F01 of Notrebamel library
from strain PEST of Anopheles gambiae (African malaria mosquito),
sequence tagged site.
AL140569 GI:6998687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission

Direct Submission

Submitted (16.FB22000) Genoscope - Centre National de Sequencage :

BP 191 91006 EYRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

- Web : www.genoscope.cns.fr)

- C hoases 1 to 900)

Roth, C.W., Brey, P.T., Ke, Z., Collins, F.H. and Weissenbach, J. Direct Submission
                                                                                                                                                                                                                                                                                                                    Homo sapiens Sukaryotas, Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryotas, Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 783) Obata, Y. Breast, gastric and prostate cancer associated antigens and uses therefor
                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (16-FEB-2000) BBMI, Institut Pasteur, 25, rue du Dr. Roux, Paris 75015, France
This clone is from an A. gambiae BAC library provided by F.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      African malaria mosquito.
Anopheles gambiae
Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Nematocera;
Culicoidea; Anopheles.
1 (bases 1 to 900)
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                                                            Length 748;
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Pred. No. 1.8e+03;
3; Mismatches 0; Indels
   3 others
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                                                                                          Indels
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                                                          Score 13.8; DB 53;
Pred. No. 1.8e+03;
3; Mismatches 0;
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LUDWIG INSTITUTE FOR CANCER RESEARCH (US)
LOCATIOn/Qualifiers
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   193 t
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Sequence 312 from Patent WO0073801.
AX053546
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/db_xref="taxon:9606"
147 c 160 g 216
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   168
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80.0%;
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Best Local Similarity 80.0%;
Acc 12; Conservative
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Best Local Similarity 80.0
Matches 12; Conservative
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46 GCTCCACTTACTCCA 32
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1 (bases 1 to 979)
Richardson,J.E., Fay,M.F., Cronk,Q.C., Bowman,D. and Chase,M.W.
A phylogenetic analysis of Rhamnaceae using rbcL and trnL-F plastid
DNA sequences
                                                                                                                                                                                                                                                                                                                                                                  ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IGS; intergenic spacer; transfer RNA-Leu (UAA); transfer RNA-Phe; tRNA-Leu (UAA) gene; tRNA-Phe gene.
Reissekia smilacina.
Chloroplast Reissekia smilacina
Eukaryota: Viridiolantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Rosales; Rhamnaceae; Reissekia.
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Richardson J.E.
Direct Submission
Submitted (28-OCT-1999) Richardson J.E., Herbarium, Royal Botanic
Garden, Edinburgh, 20A Inverleith Row, Edinburgh, EH3 5LR, UNITED
KINGDOM
                                                                                                                                                                                                                                                                                                                                                                  Gaps
Collins and sequenced by Genoscope in collaboration with the Laboratory of Biochem. and Biol. Molec. of Insects, Institut Pasteur.
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Pred. No. 1.8e+03;
3; Mismatches 0;
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/organelle="plastid:chloroplast"
/db_xref="taxon:106700"
/country="Brazil"
<1..596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="tRNA-Leu(UAA)"
/product="transfer RNA-Leu(UAA)"
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/gene="tRNA-Leu(UAA)"
597...945
/note="intergenic spacer, IGS"
                                                                                                        /organism="Anopheles gambiae"
/strain="PEST"
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                                                                                                                                                                                                                                    307
                                                                                                                                           /db_xref="taxon:7165"
/clone="0.2F01"
/clone_lib="NotreDame1"
/note="end: SP6"
a 169 c 159 g 307
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547. .596
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/gene="tRNA-Phe"
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AJ390345.1 GI:9968789
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80.0%;
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Best Local Similarity 80.0
Matches 12; Conservative
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REFERENCE AUTHORS

TITLE

AUTHORS JOURNAL

FEATURES

JOURNAL REFERENCE

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/product="interleukin-12 receptor"
/protein_id="AAR73397.1"
/db_xref="G1:8132799"
/db_xref="G1:8132799"
/translation="GPQDDDFESCLCPLEMNVAGEFQLRRRRLGSQGSSWSKWSSPVC
VPPENPOROPORPRESCHOPLEDFRRRJTLKQQPTQLELPRGCQGPAPGAEVTYQLQLHM
LSCPCKAKATRTLPLEKMPYLSGAATWMLVISSNRFGLAQTRRGTFLLTPTQKPGVLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CNSO1KVY 748 bp DNA STS 17-FEB-2000 Anopheles gambiae STS SP6 end of clone 17P09 of NotreDamel library from strain PEST of Anopheles gambiae (African malaria mosquito),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (16-FEB-2000) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
Arredondo,J.
Direct Submission
Submitted (24-JAN-2000) California Regional Primate Research
Center, University of California-Davis, One Shields Avenue, Davis,
CA 95616, USA
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Submitted (16-FEB-2000) BBMI, Institut Pasteur, 25, rue du Dr. Roux, Paris 75015, France
This clone is from an A. gambiae BAC library provided by F.H. Collins and sequenced by Genoscope in collaboration with the Laboratory of Biochem. and Biol. Molec. of Insects, Institut
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Eukaryota: Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Nematocera;
                                                                                                                                     /organism-"Macaca mulatta"
/db_xref="taxon:9544"
/db_type="peripheral blood mononuclear cells"
<1. ~487
/gene="IL-12R"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 487;
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Pred. No. 1.8e+03;
3; Mismatches 0;
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/clone_lib="NotreDame1"
/note="end : SP6"
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                                                                                                       Location/Qualifiers
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AL148863.1 GI:7007009
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Perryota; Neoptera; Endopterygota; Hymenoptera; Apocrita;
Aculeata; Formicidae; Myrmicinae; Leptothorax.
1 (bases 1 to 271)
Bruford,M.W., Green,H.A.A. and Bourke,A.F.G.
Parentage, reproductive skew and queen turnover in a multiple-queen ant analysed with microsatellites
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Direct Submission
Submitted (19-SEP-198) Conservation Genetics Group, Institute of
Zoology, Regent's Park, London NW1 4RY, UK
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AF227552 487 bp mRNA PRI 01-JUN-2000
Macaca mulatta interleukin-12 receptor (IL-12R) mRNA, partial cds
AF227552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Cercopithecidae; Cercopithecidae; Macaca. (Cercopithecidae; Macaca. 1 (bases 1 to 487)
                                                                                                                                                                                                                                                                                               Leptothorax acervorum microsatellite LXA GA 1, complete sequence. 0772036
                                                                                                         Gaps
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                                                              Length 179;
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                                                                                                       Indels
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/db_rref="taxon:33409"
                                                          Score 13.8; DB 95;
Pred. No. 1.8e+03;
3; Mismatches 0;
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Pred. No. 1.8e+03;
3; Mismatches 0;
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/rpt_type=tandem
/rpt_unit=ag
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/note="LXA GA 1"
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80.0%;
                                                              92.0%;
80.0%;
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Best Local Similarity 80.0
Matches 12; Conservative
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137 GCTCCATTTACTCCA 123
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211 GCTCCACTTGCTCCA 197
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Macaca mulatta
                                                              Query Match
Best Local Similarity
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AF227552/c LOCUS

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BASE COUNT

ORIGIN

DEFINITION ACCESSION

SOURCE ORGANISM

KEYWORDS

VERSION

AUTHORS TITLE JOURNAL REFERENCE

REFERENCE

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Gaps

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Gorman, D.M., Itoh, N., Jenkins, N.A., Gilbert, D.A., Copeland, N.G. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 179)
DiSanto, J. P., Certain, S., Wilson, A., MacDonald, H.R., Avner, P., Fischer, A. and de Saint Basile, G.
The murine interleukin-2 receptor gamma chain gene: organization, chromosomal localization and expression in the adult thymus
Bur. J. Immunol. 24 (12), 3014-3018 (1994)
                                                                                                                                                                                          Chromosomal localization and organization of the murine genes encoding the beta subunits (AIC2A and AIC2B) of the interleukin 3, granulocyte/macrophage colony-stimulating factor, and interleukin
                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 160)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus sp. liver BALB/c.
Mus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                           M95509.1 GI:191832
GM-CSF receptor B-subunit; IL-3 receptor B-subunit; IL-5 receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     General staff at the National Library of Medicine created this entry (NCBI gibbsq 161704] from the original journal article. This sequence comes from Fig. 2 and 3. Map location: X region 40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IL-2R gamma -interleukin-2 receptor gamma chain [mice, BALB/c, liver, Genomic, 179 nt, segment 5 of 8]. $75849 S75849.1 GI:861551
              LOCUS MUSAIC2B10 160 bp DNA ROD 27-APR-1993 DEFINITION MUS MUSCULUS IL-3, IL-5, and GM-CSF receptor B-subunit (AIC2B)
                                                                                                         Mus musculus (strain BALB/c, sub_species domesticus) DNA.
Mus musculus
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Pred. No. 1.8e+03;
3; Mismatches 0;
                                                                                                                                                                                                                                       J. Biol. Chem. 267, 15842-15848 (1992)
92348451
                                                                                                                                                                                                                                                                                                 /strain="BALB/c"
/sub_species="domesticus"
/db_xref="taxon:10090"
| 1. 160
/qene="AIC2B"
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/organism="Mus musculus"
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/organism="Mus sp."
/db_xref="taxon:10095"
a 37 c 50 g 4
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132 GCTCCACTTGCTCCA 118
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                                      gene, exon 10.
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Matches 12; Conserv
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                                                                                   B-subunit.
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                                                                              AF25053 Influenza
AF250563 Influenza
AF250364 Influenza
BC004691 Mus muscu
U86144 Influenza A
U86145 Influenza A
M27970 Influenza A
M27970 Influenza A
M27970 Influenza A
U53166 Influenza A
U53166 Influenza A
U53164 Musculu
AR072026 Sequence
L20048 Mouse inter
X7537 M.musculus
X66722 Bacteriopha
AF056218 Bos tauru
AF077299 Drosophil
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AR052275 Sequence
AR059955 Sequence
AR068104 Sequence
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AF086906 Arabidops
X52188 Xenopus fyn
                                                          AJ297692 Homo sapi
AF072549 Danio rer
                          M26253 Bacteriopha
                                      AF064721 Mus muscu
D13821 Mouse mRNA
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AL137281 Homo sapi
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A79383 Sequence 12
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Stinchcomb,D.T. and McSwiggen,J.A.
Interleukin-2 receptor gamma-chain ribozymes
Patent: US 5807743-A 809 15-SEP-1998;
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Pred. No. 1.9e+03;
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Sequence 809 from patent US 5807743.
AR039961
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RSM390345
CEUZ1854
PT4G11A
AF064721
MUSIL2RGAM
HSA297692
AF072549
AF072549
                                                                                            AF250363
AF250364
BC004691
IAU86144
IAU86145
FLAHANENJ8
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IAU53166
MUSIL2RGA
AR072026
MUSIL2RG
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AR097221
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A79383
AF056026
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XLFYNR
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AF056218
AF077299
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Best Local Similarity 80.0
Matches 12; Conservative
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17 GCTCCATTTACTCCA 3
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 Unknown.
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DEFINITION

AR039961/c

COCUS

BASE COUNT ORIGIN

AUTHORS TITLE JOURNAL

FEATURES

ORGANISM REFERENCE

KEYWORDS SOURCE

VERSION

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Gaps

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15-JUN-1995

44

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48

BASE COUNT

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RESULT

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Sequence:

Run on:

Searched:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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CNSO1KVY
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          GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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M95509 Mus musculu S77849 LL-2R gamma V72036 Leptothorax AF227552 Macaca mu AL148863 Anopheles AX053546 Sequence AL140569 Anopheles

AR039961 Sequence

Description

SUMMARIES

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A cDNA library of PHA-activated peripheral blood mononuclear cells in vector pEF-BOS was screened for interleukin-12 (IL-12) receptor cDNAs by panning. An isolated cDNA was sequenced (AAQ83844); it encoded a 662-amino acid low affinity IL-12 receptor (AAR69632). Recombinant IL-12 receptor was expressed in COS cells, and can be used for therapeutic or diagnostic purposes.
                                                                                                                                                                                                                                                                                                                  DNA encoding a low affinity interleukin-12 receptor - used to
bind or scavenge IL-12 to cause immune suppression, e.g. to
suppress graft-vs-host reaction, allograft rejection or
inflammation, and to treat autoimmune conditions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2104 BP; 411 A; 624 C; 658 G; 411 T; 0 other;
                                                                                                                                                                                                                                               Chizzonite RA, Chua AO, Gubler UA, Truitt TP;
           Location/Qualifiers
65..2053
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                                                                                                                                                                                                                  (HOFF ) HOFFMANN LA ROCHE & CO AG F.
                                                                                                                                                                                                                                                                                                                                                                                           Claim 3; Page 24-27; 61pp; English.
                                                                                                                                                        93US-0094649.
93US-0094713.
94US-0248532.
                                                                                                                             94EP-0110657.
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P-PSDB; AAR69632.
                                                                                                                                                        19-JUL-1993;
19-JUL-1993;
31-MAY-1994;
                                                                                                                             08-JUL-1994;
                                                                                                 15-FEB-1995
                                                                      EP638644-A.
              Key
CDS
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Search completed: August 29, 2001, 20:16:45 Job time: 7426 sec

1 RCTCCAYTTRCTCCA 15 :|||||:||:||||| 742 GCTCCACTTGCTCCA 728

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Gaps

Query Match
92.0%; Score 13.8; DB 16; Length 2104;
Best Local Similarity 80.0%; Pred. No. 2.5e+02;
Matches 12; Conservative 3; Mismatches 0; Indels 0;

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RR 22-JUN-1999; 990S-013399.

RR 23-JUN-1999; 990S-01333.

RR 24-JUN-1999; 990S-014033.

RR 24-JUN-1999; 990S-014033.

RR 24-JUN-1999; 990S-014083.

RR 25-JUN-1999; 990S-014184.

RR 01-JUL-1999; 990S-014184.

RR 01-JUL-1999; 990S-014225.

RR 13-JUL-1999; 990S-014227.

RR 13-JUL-1999; 990S-014331.

RR 15-JUL-1999; 990S-014332.

RR 15-JUL-1999; 990S-014332.

RR 15-JUL-1999; 990S-014433.

RR 13-JUL-1999; 990S-014433.

RR 13-JUL-1999; 990S-014433.

RR 22-JUL-1999; 990S-01433.

RR
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Interleukin-12 receptor: IL-12; immune suppression; immunosuppressive; graft-versus-host reaction; allograft rejection; inflammation; autoimmune disease; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human interleukin-12 receptor cDNA.
                                                                                                                                                                                                                              99US-0159330.
99US-0159331.
99US-0159637.
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99US-0155659.
99US-0156458.
99US-0156596.
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99US-0157753.
99US-0157865.
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99US-0158369.
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99US-0159294.
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99US-0159329.
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99US-0160770.
99US-0160814.
99US-0160815.
99US-0154779
99US-0155139
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99US-0160767
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99US-0160989
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1223 ACTCCACTTGCTCCA 1209
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25-0CT-1999;
26-0CT-1999;
26-0CT-1999;
26-0CT-1999;
28-0CT-1999;
28-0CT-1999;
28-0CT-1999;
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ID AAQ838

AC AAQ838

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DE Human

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KW Interl

KW inflam

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Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
 Arabidopsis thaliana DNA fragment SEQ ID NO: 49177.
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990S-0139453.
990S-0139492.
990S-0139454.
990S-0139455.
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990S-0128714.
990S-0129845.
990S-0130077.
990S-0130449.
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99US-0132863.
99US-0134256.
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99US-0138094.
99US-0138540.
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99US-0131449.
99US-0132048.
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99US-0132484.
99US-0132485.
99US-0132486.
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99US-0134219.
99US-0134221.
99US-0134370.
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99US-0139457.
99US-0139458.
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990S-0126264.
990S-0126785.
990S-0127462.
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99US-0139750.
99US-0139763.
99US-0139817.
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99US-0135124
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                                                                     Arabidopsis thaliana.
                                                                                            EP1033405-A2
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16-JUN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAQ71977 is the DNA sequence of murine IL-2R gamma AAR59094, this was used in the development of a claimed method for the diagnosis of X-linked severe combined immunodeficiency (XSCID), in female carriers and male sufferers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 13.8; DB 15; Length 1608;
Pred. No. 2.5e+02;
Mismatches 0; Indels 0;
                                                                                                                                                   Murine IL2-R gamma; X-linked severe combined immunodeficiency; XSCID; interleukin; ss.
                                                                                                                                                                                                                                   /*tag= a
/transl_except= pos:1015..1017, aa:His
25..82
/*tag= b
/note= "Putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1608 BP; 413 A; 434 C; 349 G; 412 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                 (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Leonard WJ, Mcbride WO, Noguchi M;
                                                                                                                                                                                                             Location/Qualifiers
25..1134
                                                        AAQ71977 standard; DNA; 1608 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAC46177 standard; DNA; 2061 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 1; Fig 7; 98pp; English.
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80.0%;
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93US-0121435
                                                                                                      03-MAY-1995 (first entry)
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Best Local Similarity 80.0
Matches 12; Conservative
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750 GCTCCATTTACTCCA 736
891 GCTCCACTTACTCCA 877
                                                                                                                            Murine IL-2R gamma gene.
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P-PSDB; AAR59094.
                                                                                                                                                                                      Mus musculus
                                                                                                                                                                                                                                                                                                                                                       10-MAR-1994;
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14-SEP-1993;
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                                                                                                                                                                                                                                                             sig_peptide
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                                                                               AAQ71977;
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                                             AAQ71977,
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	x x x x x x x x x x x x x x x x x x x		RARARA XARARA XA

Score 13.8; DB 21; Length 1537; Pred. No. 2.5e+02; 3; Mismatches 0; Indels 0; Query Match 92.0%; Best Local Similarity 80.0%; Matches 12; Conservative 3 990S-0148171.
990S-01481319.
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990S-0148365.
990S-0149172.
990S-0149722.
990S-0149723.
990S-0149723.
990S-0149723.
990S-0149723.
990S-0149930.
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990S-015923.
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Gaps

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Gaps

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Length 1414; Indels

Matches

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Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
                                                                                                                                                                                                                                                                                                                                               Arabidopsis thaliana DNA fragment SEQ ID NO: 13639.
                                     92.0%; Score 13.8; DB 19; 80.0%; Pred. No. 2.5e+02;
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0
                                                                         3; Mismatches
                                                                                                                                                                                                                                      AAC36394 standard; DNA; 1537 BP.
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99US-0126785.
99US-0127462.
99US-0128234.
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99US-0134256.
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                                                                                                                                                                                                                                                                                                           17-OCT-2000 (first entry)
                                                                                                                               1037 ACTCCATTTGCTCCA 1023
                                                      Best Local Similarity 80.0
Matches 12; Conservative
                                                                                                          1 RCTCCAYTTRCTCCA 15
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                                                                                                                                                                                                                                                                       AAC36394;
                                       Query Match
                                                                                                                                                                                                  RESULT 12
AAC36394/c
                                                                                                                                              q
                                                                                                              δλ
                                                                                                                                                                                                                                                          The present sequence represents SEQ ID NO:228 from the present invention, this sequence is only given in the sequence listing and is not mentioned further in the specification. The present invention specifically describes recombinant swinepox virus (SPV) comprising a foreign DNA (I) inserted into a SPV CC genome which is capable of being expressed in a cost call into which the virus is introduced, where (I) is inserted into:

(a) an EcoRI site within a region corresponding to a 3.2 kb subfragment of the HindIII K fragment which contains both a HindIII and an ECORI site, of the SPV genome, and optionally (b) an AccI site within a region corresponding to a 3.6 kb HindIII we be used in a vaccine for immunising an animal against SPV. The invention also provides a method for testing a corresponding to a 3.6 kb HindIII to BgIII subfragment of the HindIII M fragment. The recombinant SPV can be used in a vaccine for immunising an animal against SPV. The invention also provides a method for testing a content, particularly containing S-SPV-008, or is infected with a content of determine whether the swhne has been vaccined with a courring wild-type pseudorabies virus. Also (I) inserted into containing SPV can be used in a diagnostic assay, e.g. Feline immunications and Dirofilaria immitis contained by and 22kd are useful to detect feline immunodeficiency caused by FIV can be immitis respectively.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /*tag- a /*tag- a // note- "encodes protein given in AAW55998; a stop codon is given in between amino acids at the end of the protein"
                                     Gaps
                                                                                                                                                                                                                                                                                                                                           Swinepox virus; SPV; recombinant; vaccine; immunisation; diagnosis; pseudorabies virus; feline immunodeficiency virus; FIV; heartworm;
                                                                                                                                                                                                                                                                                                         Genomic DNA SEQ ID NO:228 from WO9804684 encoding SEQ ID NO:229.
                                     ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Recombinant swine pox virus - useful in vaccine for immunising
Sequence 1414 BP; 463 A; 253 C; 324 G; 374 T; 0 other;
                                     3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 402-405; 473pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
1..1414
                                                                                                                                                                                                AAV26248 standard; DNA; 1414 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      animal against swine pox virus
                80.08;
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                                                                                                                                                                                                                                                                      24-JUL-1998 (first entry)
                                   12; Conservative
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803 GCTCCACTTACTCCA 789
                                                                                                                                                                                                                                                                                                                                                                                Dirofilaria immitis; ss.
                                                                       1 RCTCCAYTTRCTCCA 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1998-130677/12.
                  Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P-PSDB; AAW55998
                                                                                                                                                                                                                                                                                                                                                                                                                    Unidentified
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-JUL-1997;
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                                                                                                                                                                                                                                  AAV26248;
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	92.0%; Score 13.8; DB 21; Length 1290;
PR 05-AUG-1999; PR 06-AUG-1999; PR 09-AUG-1999; PR 10-AUG-1999; PR 10-AUG-1999; PR 11-AUG-1999; PR 12-AUG-1999; PR 13-AUG-1999; PR 13-AUG-1999; PR 13-AUG-1999; PR 22-AUG-1999; PR 23-AUG-1999; PR 23-AUG-1999; PR 23-AUG-1999; PR 24-SEP-1999; PR 25-AUG-1999; PR 27-AUG-1999; PR 28-AUG-1999; PR 29-AUG-1999	Query Match
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77528 888540 994544 994546 994552 994553 994557 994653 994657 994657 994657 994657 994657 994657 994657 994657 994657 994657 994657 994657 994657 994657 994657 994657 99557	7192.
99005-0137 99005-0137 99005-0137 99005-0137 99005-0138 99005-0139	90S-014
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polynucleotides, based on which tissues they are most highly expressed
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                                                                                Length 1217;
                                                                                                          Indels
                                        G; 416 T; 0 other;
                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana DNA fragment SEQ ID NO: 58287.
                                                                            Score 13.8; DB 20;
Pred. No. 2.4e+02;
3; Mismatches 0;
                                        Sequence 1217 BP; 346 A; 232 C; 223
             (see AAZ24811 for described uses)
                                                                                                                                                                                                                               . AAC48659 standard; DNA; 1290 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99US-0127462.
99US-0128234.
99US-0128714.
99US-0129845.
                                                                               92.0%;
80.0%;
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99US-0123548.
99US-0125788.
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99US-0130891.
99US-0131449.
99US-0132048.
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99US-0126785
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99US-0134218
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                                                                                                                                                                                                                                                                                    (first entry)
                                                                         Query Match
Best Local Similarity 80.0° Matches 12; Conservative
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1076 ACTCCACTTGCTCCA 1062
                                                                                                                                   1 RCTCCAYTTRCTCCA 15
                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                    EP1033405-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-MAR-1999;
01-APR-1999;
06-APR-1999;
08-APR-1999;
16-APR-1999;
                                                                                                                                                                                                                                                                                  18-OCT-2000
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                                                                                                                                                                                                                                                         AAC48659;
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                                                                                                                                    δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence represents a nucleic acid molecule which encodes a secreted human protein. The gene number, and the clone it is derived from, are detailed in the descriptor line. The gene can be used to generate fusion proteins by linking to the gene to a human immunoglobulin Pc portion (e.g. AA224802) for increasing the stability of the fused protein as compared to the human protein only.

The invention relates to 95 novel genes and their fragments (nucleic acid sequences: AA224811-224907; amino acid sequences AAY41308-Y41404) which are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Also, pathological conditions can be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the new polynucleotides. Specific uses are described for each of the 95
                                                                                                                                                                                                  Human; secreted protein; fusion protein; gene therapy; protein therapy; diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia; developmental abnormality; foetal deficiency; blood; allergy; renal; ds; immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma; inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS; cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus; osteoporosis; arthitiis; testis; lung; thyroiditis; thyroid; digestion; endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated human genes, useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Soppet DR;
Ir DW;
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, Lafleur
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rosen CA, Yu G, Young PE, Fer
A, Duan RD, Kyaw H, Ebner R,
Moore PA;
                                                                                                                                                                          Human secreted protein gene 26 clone HPMFP40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 314; 484pp; English.
                                                                              AA224836/c
ID AA224836 standard; DNA; 1217 BP.
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98US-0078573.
98US-0078574.
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98US-0080312
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                                                                                                                                               (first entry)
1 RCTCCAYTTRCTCCA 15
             Wei Y, Endress GA,
Olsen HS, Shi Y, M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1999-562050/47.
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01-APR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ruben SM,
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WO200073801-A2
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10-SEP-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                    07-DEC-2000
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                                                                                                                                                                                                                   AAF22733/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence encodes a polypeptide which is associated with the exocytosis pathway. CDNA molecules encoding proteins involved in exocytosis have been isolated by yeast one-hybrid and two-hybrid screening. Novel proteins, termed Exo proteins, have been identified that interact with known exocytosis-associated proteins such as GS27, alpha snap, uncl8-1, vamp3, snap-23, and the rab family of proteins. Exo proteins and their agonists and antagonists are useful in the diagnosis, treatment or prevention of exocytosis-mediated disorders such as asthma, inflammation, allergies, Chediak-Higashi Syndrome (CHS), Alzheimer's disease, Parkinson's disease, Huntington's disease,
                                                                                                                                                                                                                                                                                  Exocytosis pathway protein; Exo protein; antiparkinsonian; antidiabetic; antiallergic; antiasthmatic; nootropic; neuroprotective; anticonvulsant; vulnerary; asthma; inflammation; allergy; Chediak-Higashi syndrome; CHS; Alzheimer's disease; Parkinson's disease; Huntington's disease; diabetes; digestion disorder; wound healing disorder; gene therapy; ss.
allergy and other inflammatory conditions. The ribozymes are also used to induce tolerance in a recipient to alloantigen from a donor.
                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New nucleic acids encoding Exo proteins which are useful in the diagnosis, treatment or prevention of exocytosis-mediated disorders such as asthma, inflammation and allergies - .
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                                                                  Length 17;
                                                                                         Indels
                                                                   DB 19;
                                                                 Score 13.8; DB 19;
Pred. No. 1.8e+02;
3; Mismatches 0;
                                 Sequence 17 BP; 6 A; 1 C; 7 G; 3 U; 0 other;
                                                                                                                                                                                                                                                              Mouse IL-3 receptor nucleotide sequence #3.
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                                                                                                                                                                                            BP.
                                                                                                                                                                                          AAA89732 standard; cDNA; 494
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990S-0117308.
990S-0117319.
990S-0118177.
990S-0118177.
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99US-0119998.
99US-0119759.
                                                                 Query Match 92.0%;
Best Local Similarity 80.0%;
Matches 12; Conservative
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                                                                                                                                                                                                                                        (first entry)
                                                                                                              1 RCTCCAYTTRCTCCA 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (RIGE-) RIGEL PHARM INC
                                                                                                                          WPI; 2000-482908/42.
                                                                                                                                                                                                                                                                                                                                                                             WO200043419-A2.
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26-JAN-1999;
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                                                                                                                                                                                                                  AAA89732;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 condition characterised by expression of an abnormal amount of a protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human gastric cancer associated antigen nucleotide sequence SEQ ID:312.
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                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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diabetes, digestion disorders and wound healing disorders. The nucleic acids, antagonists or agonists of Exo proteins are use in gene therapy. The nucleic acids are also useful for generating transgenic or knock-out animals which can be used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; breast cancer; gastric cancer; prostate cancer; diagnosis; cancer associated antigen; cytostatic; cancer vaccine; ss.
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                                                                                                                                                                                                                                                                                                                Score 13.8; DB 21; Length 494; Pred. No. 2.3e+02;
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                                                                                                                                       development and screening of therapeutically useful reagents.
                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                             Sequence 494 BP; 125 A; 135 C; 129 G; 101 T; 4 other;
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                                                                                                                                                                                                                                                                                                                                                                                          3; Mismatches
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                                                                                                                                                                                                                                                                                                                92.0%;
80.0%;
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99US-0153454.
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                                                                                                                                                                                                                                                                                                                                                                                      12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          231 GCTCCACTTGCTCCA 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 RCTCCAYTTRCTCCA 15
                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
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The invention relates to the isolation of sequences encoding human haemopoietin receptor protein family NRB genes. The NRB family sequences were initially searched for comparison on a nucleic acid database with the nucleic acid probe sequence TGGAGYNNNTGGAGY encoding the amino acid sequence Trp-Ser-Xaa-Trp-Ser. The sequences AAZ59288-253300 and AAZ992816-290925 represent specific axamples of probe sequences used in the search. Antibodies to the NRB family proteins are used for the diagnosis of blood formation disorders. Compounds identified
                                                                                                                                                                                                                                                                                                                                       as binding to the proteins are used for the treatment of such disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence invention describes ribozymes targeted to modulate the synthesis and/or expression of interleukin (IL)-2R gamma encoded RNA. AAV93889 to AAV94574 represent specifically claimed ribozymes, and AAV94575 to AAV95260 represent specifically claimed substrate sequences from the present invention. The ribozymes can be used for the treatment of, e.g. graft rejection, autoimmune disease, cancer, psoriasis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; IL-2 receptor g-chain; interleukin 2 receptor gamma chain; hammerhead ribozyme; hairpin ribozyme; substrate; expression; cancer; autoimmune disease; psoriasis; allergy; inflammatory disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                             Hemopoletin receptor protein family NR8 used for diagnosis of blood
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ribozymes targeted to interleukin 2 - useful for treating e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mouse IL-2 receptor g-chain substrate position 725.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 13.8; DB 21;
Pred. No. 1.7e+02;
                                                                                                                                                                                                                                                                                                                                                                           Sequence 15. BP; 4 A; 1 C; 7 G; 3 T; 0 other;
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                                                                                                                                      Example 1; Page 45; 176pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     92.0%;
80.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (RIBO-) RIBOZYME PHARM INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12; Conservative
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15 ACTCCACTTGCTCCA 1
                                    WPI; 2000-116933/10.
                                                                                                  formation disorders
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Maeda M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best_Local Similarity
Matches 12; Conserv
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  Nomura H,
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Haemopoietin receptor family; NR8; antibody; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Haemopoletin receptor family; NRB; antibody; diagnosis; blood formation disorder; fusion protein; probe; ss.
                blood formation disorder; fusion protein; probe; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 13.8; DB 21;
Pred. No. 1.7e+02;
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                                                                                                                                                                                                                                                                         CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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80.0%;
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98JP-0297409
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98JP-0297409
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AAZ90914 standard; DNA; 15
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Best Local Similarity 80.0
Matches 12; Conservative
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                                                                                                                                                                                                                                                                                                                  Maeda M;
                                                           Homo sapiens
                                                                                              WO9967290-A1
                                                                                                                                                                         23-JUN-1999;
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19-OCT-1998;
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Haemopoietin receptor family; NR8; antibody; diagnosis; blood formation disorder; fusion protein; probe; ss.
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                                                                                                                                                       AAZ90874 standard; DNA; 15
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                           1 RCTCCAYTTRCTCCA 15
                                              WPI; 2000-116933/10
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                                                                                                                                                                                                                                                                                     Gaps
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                                    5 Degenerate hybridisation probes (AAT17870-74) are based on a conserved motif (AAR92812) found in haemopoietin receptors. The probes are used in the identification and/or cloning of genes coding for novel haemopoietin receptors, e.g. the murine interleukin-11 (IL-11) receptor alpha chain gene (AAT17868) receptors are defined by their ability to hybridise to the probes under medium stringency conditions.
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                                                                                                                                                                                          Sequence 15 BP; 2 A; 6 C; 0 G; 4 T; 3 other;
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Claim 12; Page 52; 87pp; English.
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99WO-JP03351

98JP-0297409 98JP-0214720

Maeda M;

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Hemopoietin receptor protein family NR8 used for diagnosis of blood formation disorders - \,
                                                                                                                              The invention relates to the isolation of sequences encoding human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  92.0%; Score 13.8; DB 21; Length 15; 80.0%; Pred. No. 1.7e+02;
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AAZ90907/c
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92.0%; Score 13.8; DB 21; ilarity 80.0%; Pred. No. 1.7e+02; Conservative 3; Mismatches 0;

Query Match Best Local Similarity Matches 12; Conserv

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Human NRB gene pro
Human NRB gene pro
Mouse IL-2 recepto
Mouse IL-3 recepto
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Human secreted pro
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Human NR8
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**SIDSB/gcgdata/geneseq/geneseqn/NA1981.DAT:**

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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·	37	. m		436	21	AAC01348	Human secreted p
0 0	80 G 60 F	m m	œ œ	480	212	AAC01349 AAC43764	Human secreted pr
0	40	· m		762	21	AAA26722	ğ
O	41		œ æ	1485	21	AAC42934 AAC36662	Arabidopsis thal
	43	. n		151826	21	AAF22291	BAC containing re
U	44 45	2.5		17 30	19 20	AAT94135 AAX87693	Probe 9560 for ha Human TPST-1 CDN
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RES AAT ID	RESULT AAT17874 ID AAT1	1 17874 s	tandard;	; DNA;	15 B	ū	
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DT	21-N	-MAY-199	6 (fir	st entry	γ)		
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XXX	Наеп	+	: u	interleukin	- 7	: receptor:	adonist: antadonist:
X X	ther	, –	iagn	s; probe	١		
SO	Synt	Synthetic.					
XX N	WO96077	37	-A1.				
XX Od	14-1	-MAR-199	. 9				
XX PF	05-5	SEP-199		95WO-AU0057	578.		
×							
A A >	05-8	SEP-199. SEP-199	4; 94	AU-0007	902. 901.		
PA	(AMRA	·	AMRAD OPE	OPERATIONS	PTY	LTD.	
PI	Hilt	ton DJ;					
DR.	WPI;	1996	-171612/	/17.			
XX Td	Nucl	Nucleic aci	id enco	ding esp.	haemopoie IL-11 rec	oietin receptor containing c receptor alpha chain - used	ing conserved used for
PY XX	deve	loping	IL-1	(ant)	onis		

in a manual manu

us-09-532-263-10.rst

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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Vector: lambdaphage SHLX2; Mixed stage
hermaphrodite cDNA library. Partially normalized by
successively picking groups of clones that didn't
hybridize to previously picked clones. Vector: lambdaphage
SHLX2 (Lipshitz, D.H. et al., Gene 88:25-36 (1990)) Host:
MC1061"
                                                                                                                                     Contact: Waterston R.H.(USA) and Sulston J.E.(UK)
(USA) Dept. of Genetics or (UK)
(USA) Washington Univ. School of Medicine or (UK) MRC Laboratory of
Molecular Biology
Box 8232,4566 Scott Ave., St. Louis, MI 63110, USA, or, Hills Road
, Cambridge CB2 2QH, UK
Tel: (USA) (314)3627072 or (UK) (0223)248011
Fax: (USA) (314)3624137 or (UK) (0223)402008
Email: rw@nematode.wustl.edu or jes@mrc-lmba.cambridge.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 324)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
,L., Durbin,R.K., Green,P., Shownkeen,R., Halloran,N., Hawkins,T., Wilson,R., Berks,M., Du,Z., Thomas,K., Thierry-Mieg,J. and Sulston

        BF936011
        324 bp
        mRNA
        EST
        22-JAN-2001

        L2-WT0198-291200-291-B05 NT0198 Homo sapiens cDNA, mRNA sequence.
        BF936011
        GI:12353335

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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Shotgun sequencing of the human transcriptome with ORF expressed
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Pred. No. 2.4e+03;
3; Mismatches 0; Indels 0;
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/organia-"caenorhabditis elegans"
/strain-"Bristol N2"
/db_xref-"taxon:6239"
/clone-"cm21f0"
/lone_lib-"Chris Martin sorted cDNA library"
/lab_host-"MC1061"
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20202663
                                                                     survey of expressed genes in Caenorhabditis elegans ture Genet. 1, 114-123 (1992)
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                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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80.0%;
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Fax: +55-11-2707001
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Best Local Similarity 80.0
Matches 12; Conservative
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BF936011/c
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Nr0198"
/dev_stage="Adult"
/note="Organ: nervous_tumor; Vector: puc18; Site_l: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
10 thers
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This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL2&t2=IL2-NT0198-291200-291-B05&t3=2000-12-29&t4=1)
Seq primer: puc 18 forward.
High quality sequence stop: 72.
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80.0%; Pred. No. 2.4e+03;
iive 3; Mismatches 0; I
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RESULT 12

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B75501/c

ORGANISM

REFERENCE AUTHORS

TITLE JOURNAL

COMMENT

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Caenorhabditis elegans.
Caenorhabditis elegans
Caenorhabditis elegans
Eukaryota: Metazoa: Nematoda; Chromadorea; Rhabditida; Rhabditoidea
; Rhabditidae: Peloderinae; Caenorhabditis.
1 (bases 1 to 324)
Waterston, R., Martin, C., Craxton, M., Huynh, C., Coulson, A., Hillier
                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

( pases 1 to 305)

Mahairas,G.G., Zackrone,K.D., Smith,T., Tipton,S., Schmidt,S., Traicoff,R., Abajian,C., Blanchard,A., West,A. and Hood,L.E. Construction of a Characterized Clone Resource for Genomic Sequencing: Generation and Preliminary Analysis of 20,000 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MB9352 324 bp mRNA EST 16-SEP-1992
CELLIF10 Chris Martin sorted cDNA library Caenorhabditis elegans
CDNA clone cm21f10 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in E-Coli DH10B"
                                                                                                                                                                                                               B40700 305 bp DNA GSS 18-OCT-1997 HS-1052-A1-E09-MF.abi CIT Human Genomic Sperm Library C Homo saplens genomic clone Plate=CT 774 Col=17 Row=I, DNA sequence. B40700. GI:2544952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
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/dlone="piate=Cr 774 Col-17 Row=I"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tagged Connectors
Unpublished (1997)
Contact: Mahairas GG, Zackrone KD, Hood L
University of Washington
Seatile, WA 98195, USA
Tel: (206) 616-8744
Fax: (206) 685-7301
Email: kzackron@u.washington.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 13.8; DB 256;
Pred. No. 2.4e+03;
3; Mismatches 0;
      Pred. No. 2.4e+03; 3; Mismatches 0
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Plate: CT 774 row: I column: 17
Class: BAC ends
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Location/Qualifiers
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                          12; Conservative
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Other-GSSs: Rectil-16K9.TP
Contact: Mark Adams
Contact: Mark Adams
Contact: Mark Adams
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0200
Fax: 301 838 object of Genomic Research
Glones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong
(pleter Gelpong med. buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genetics (info@researcn). BAC end search page:
http://www.igr.org/tdb/humgen/bac_end_search/bac_end_search.html
                                                             ö
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contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAAGGAGGAAGGACTCTTTTTTTTTTTTTTVN 3'], cDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 291)
Adams,M.D., Rounsley,S.D., Field,C.E., Bass,S., Linher,K., Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., de Jong,P. and Venter
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/sex="Male"
/cell_type="Lymphocytes"
/note="Vector: pBACe3.6; Site_l: EcoRI; Site_2: EcoRI;
RPCIl1 Human Male BAC Library"
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pred. No. 2.4e+03;
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/db_xref="GDB:7506008"
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80.0%;
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                                               Monno, H., Aizawa, K., Akahira, Stanioginchii, Mulindasi Mulinda, Muse.

Konno, H., Aizawa, K., Akahira, S., Akiyama, J., Arakawa, T., Carninci
, P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsı, N.,
Hirozane, T., Hori, F., Ishi, Y., Ishikawa, J., Ishikawa, T., Itoh, M.,
Izawa, M., Kadota, K., Kagawa, T., Kai, C., Kakuchi, N.,
Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kusakabe, M.,
Matuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y.,
Ono, T., Owa, C., Salto, H., Sakai, C., Sato, K., Shibata, Y., Suguki, H., Sauki, T., Taqawa, A., Takahashi, F., Tominaga, N., Toya
, Y., Shigemoto, Y., Shinagawa, A., Takahashi, F., Tominaga, N., Toya
, T., Tsunoda, Y., Watahiki, A., Yokahashi, F., Tominaga, N., Toya
, T., Yano, R., Yasunishi, A., Yoka, T., Yamamura, T., Yamanaka, I.,
Yano, R., Yasunishi, A., Yoka, T., Yoshino
RIKEN Mouse Ests (Ronno, H., et al.)
Unpublished (2000)
Contact: Yoshihide Hayashizaki
Genome Exploration Research Group, Life Science Tsukuba Center,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: genome-resertc.riken.go.jp,
URL:http://genome-rtc.riken.go.jp,
carninci.p., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki,Y., Y. and Hayashizaki,Y.
Automated filtration-based high-throughput plasmid preparation System. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
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/lab_host="DH100"
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                              Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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The Institute of Physical and Chemical Research (RIKEN), Genomic
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/db_xref-"taxon:10090"
/clone="C530024L16"
/clone=lib-"RIKEN full-length enriched, 12 days embryo spinal cord"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: +81-298-36-9013
Fax: +81-298-36-9098
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Location/Qualifiers
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                                                                                               AUTHORS
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DB 133; Length 272;

Score 13.8; DB 13. Pred. No. 2.4e+03;

92.0%; 80.0%;

Query Match Best Local Similarity

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Alzawa, K., Akahira, S., Akimura, T., Arai, A., Arakawa, T., Carninci, P., Hanagaki, T., Hayatsu, N., Hiraoka, T., Hirozane, T., Hodoyama, Y., Imanai, Y., Ishii, Y., Itoh, M., Izawa, M., Kawai, J., Kojima, Y., Konno, H., Kusakabe, M., Marayama, T., Miyazaki, A., Nakamura, Y., Konno, H., Kusakabe, M., Matsuyama, T., Miyazaki, A., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Sabaki, R., Shibata, Y., Shibata, Y., Shibata, Y., Shibata, Y., Shinagawa, A., Takahashi, Y., Shinagawa, A., Takahashi, T., Toya, T., Watahiki, A., Yamamura, T., Yasunishi, A., Yoshida, K., Yoshida, K., Elkiki, Mouse ESTS (Alzawa, K. et al. 2000)

Contact: Yoshinde Hayashizaki, Y.
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                                                                                                                                                                                                                                                                                                                                                                                                 BB585089 RIKEN full-length enriched, 12 days embryo, embryonic body between diaphragm region and neck Mus musculus cDNA clone 9430004A04 5', mRNA sequence.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 287)
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/clone_lib="RIKEN full-length enriched, 12 days embryo,
embryonic body between diaphragm region and neck"
/tissue_type="embryonic body between diaphragm region and
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Automated filtration based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
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/note="Site_1: Sal1; Site_2: BamHI; cDNA library was
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1 RCTCCAYTTRCTCCA 15
                                                               3 ACTCCACTTGCTCCA 17
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AI119961.1 GI:3520285
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214 GCTCCATTTACTCCA 200
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Mus musculus
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1 (bases 1 to 240)

1 (bases 1 to 240)

M. Miyata, N. and Nishigaki, A. Expression map of the C.elegans genome
Contact: Yuji Kohara
Gene Library Lab
National Institute of Genetics
National Institute of Genetics
Tel: 81-559-81-6884
Fax: 81-559-81-6855
                                                                              Clones from this library are designated with the
Lambda ZAP II cDNA library was constructed from mRNA extracted from etiolated leaf tissue of the rice cultivar 'IR36' and converted to pBluescript (amp resistant) as described in Causse et al. (1994) Genetics 138:1251-1274. For insert amplification, Use MI3 forward and reverse
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/db_xref="taxon:6239"
/clone="yx284c9"
hermaphrodite embryo"
/sex="hermaphrodite"
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Pred. No. 2.3e+03;
3; Mismatches 0; Indels 0:
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Pred. No. 2.3e+03;
3; Mismatches 0; Indels (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: ykohara@lab.nig.ac.jp.
Location/Qualifiers
1. .240
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Caenorhabditis elegans
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80.0%;
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167 GCTCCACTTGCTCCA 181
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Best Local Similarity
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Matches 12; Conserv
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1 (bases 1 to 248)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schallenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Organ: mammary gland; Vector: pT7T3D-Pac (Pharmacia ) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BB420958 RIKEN full-length enriched, 12 days embryo spinal cord Mus musculus cDNA clone C530024L16 3', mRNA sequence.
BB420958.1 GI:9242313
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Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                      WashU-HHMI Mouse EST Project
Washigton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty.free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:139B26"
/clone=lib="Soares_nammary_gland_NDMMG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Trace considered overall poor quality
Seq primer: -28mil rev2 ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
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/dev_stage="4 weeks"
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                                                                                                                                                                                                                                                                      Unpublished (1996)
Contact: Marra M/Mouse EST Project
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/organism="Mus musculus"
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us-09-532-263-10.rst

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Tal: 607 255 0420

Fax: 607 255 6683

Email: srm4@cornell.edu

CDNA from Trice (Oryza sativa); forward sequence of RFLP probe

RZ612. Sequence determined by Nicola M. Ayres. For mapping

information, additional citations and other related information

concerning this probe, please refer to the RiceGenes database at

http://ars-genome.cornell.edu/cgi%20bin/WebAce/Webace?db-ricegeness&
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/clone="Rx612"
/clone_lib="cDNA from rice"
/note="Vector: Lambda 2AP II/pBluescript; Site_1: EcoRI; A
                                                                                                                                                                                                                                                                                                              /lab_lost="E. coli XII-Blue"
/note="Vector: Lambda ZAP; Site_1: EcoR I; Site_2: Xho I;
/note="Vector: Lambda ZAP; Site_1: EcoR I; Site_2: Xho I;
The mouse brain library (Stratagene ) was constructed by oligo-(dT) priming and directional cloning in Uni-ZAP XR phage using whole brain mRNA from a Balb C post natal 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oryza sativa
Sukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA231776 231 bp mRNA EST 15-SEP-2000 RZ612.F cDNA from rice Oryza sativa cDNA clone RZ612, mRNA sequence.
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VanDeynze, A.E., Sorrells, M.E., Park, W.D., Ayres, N.M., Fu, H.,
Cartinhour, S.W., Paul, E. and McCouch, S.R.
Anchor Probes for Comparative Mapping of Grass Genera
Theor. Appl. Genet. 97, 356-369 (1998)
Contact: McCouch S.R.
Dept Plant Breeding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 13.8; DB 188; Length 216;
Pred. No. 2.3e+03;
3; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 others
                  Contract: Sikela JM
Contract: Sikela JM
Department of Pharmacology
University of Colorado Health Sciences Center
Box C336, 4200 E. 9th Ave, Denver CO 80262-0236
Tel: 3032708637
Fax: 3032707097
Emai: nikki@tally.uchsc.edu
Seq primer: M13 Reverse.
                                                                                                                                                                                                                                                                       /db_xref="taxon:10090"
/clone_lib="Mouse brain, Stratagene"
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/cultivar="IR36"
/db_xref="RiceGenes:RZ612"
                                                                                                                                                                                                                                               /organism="Mus musculus"
                                                                                                                                                                                                      Location/Qualifiers
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Location/Qualifiers
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Ithaca, NY 14853-1901, USA
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AA231776.1 GI:1854148
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  Unpublished (1995)
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Best Local Similarity 80.0
Matches 12; Conservative
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Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases
This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
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0
                                                                  clone
                                                                                                                                                                          GSS; genome survey sequence.
Tetraodon nigroviridis.
Tetraodon nigroviridis
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 216)
Beler, D. and Brady, K.
Mouse brain cDNAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence
                                                                                                                                                                                                                                                                                                              Tetraodontidae; Tetraodon.
1 (bases 1 to 215)
0 (boset-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weissenbach, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 (bases 1 to 215)
Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C.,
Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F.,
Saurin, W. and Welssenbach, J.
                                                                                                                                                                                                                                                                                                                                                                                                                   Charaterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
                                           CNSO32CC 215 bp DNA GSS 15-MAY-2000 Tetraodon nigroviridis genome survey sequence PUC-Ori end of clc 206N11 of library G from Tetraodon nigroviridis, genomic survey
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Stratagene Mus musculus CDNA 5'end, mRNA
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Pred. No. 2.3e+03;
; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon. Location/Qualifiers
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/db_xref="taxon:99883"
/clone="206N11"
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/note="Genoscope sequence ID
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ALZ24661.1 GI:7883532
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80.0%;
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R74725.1 GI:849928
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Simpson, A.J.
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                                                                                                                                    /clone_lib="Overy 2 (OV2)"
//clone_lib="Organ: Mix of ovaries of varying immature stages
from 8-week-old plants; Vector: pBluescript II from Lambda
Zap II; Site_l: Khol; Site_2: ECORI; The library was made
from poly-A RAB in the cloning vector lambda ZAP II.
Clones to be sequenced were prepared by mass excision."

27 c 33 g 46 t
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RPCI-11-366P19.TV RPCI-11 Homo sapiens genomic clone RPCI-11-366P19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: hbe@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genet cs (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: T7
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 186)
Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and Venter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready Map Building
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/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCI11 Human Male_BAC_Library"
                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                            Unpublished (1997)
Contact: Shaying Zhao, William Nierman, Mark Adams
Contact: Shaying Zhao, William Nierman, Mark Adams
Contact: Shaying Zhao, William Nierman, Mark Adams
The Institute for Genomic Research
The Institute for Genomic Research
The Madical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208

    154
    /organism="Sorghum bicolor"
/db_xref="taxon:4558"

High quality sequence start: 9
High quality sequence stop: 125
                                                             Location/Qualifiers
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KEYWORDS
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                                                          FEATURES
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Tel: +55-11-2704922
Fax: +55-11-2707001
Fax: +55-11-2707001
Fax: +55-11-2707001
Fax: +55-11-2707001
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl-&t2-CMO-HTO548-210 S00-233-e07&t3-2000-02-21&t4-1)
Seq primer: puc 18 forward
High quality sequence start: 2
High quality sequence start: 2
Location/Qualifiers
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Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., Gastluya, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
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Site_2: Smal; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and CDNA amplification were performed under
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Shotgun sequencing of the human transcriptome with ORF expressed
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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Pred. No. 2.2e+03;
; Mismatches 0;
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Pred. No. 2.3e+03;
3; Mismatches 0; 1
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Result No.

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E NAL L LOCAL LOCA	SOURCE Sorghum bicolor Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Sorghum. I (bases 1 to 154) AUTHORS Cordonnier-Pratt,MM., Gingle,A., Marsala,C., Sudman,M. and Pratt, L.H. TITLE An EST database from Sorghum: ovaries of varying immature stages JOURNAL Unpublished (2000) COMMENT Contact: Cordonnier-Pratt MM Department of Botany The University of Georgia Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA Tel: 706 542 1805 Email: mmpratt@uga.edu Seq primer: JEN REV
AA03844 mi83c09.r BG159502 002.5_B09 AQ554938 RPCI-11-3 BB171588 CM0-HT054 AL224661 Tetracodon R74725 MDB0891R MC AA21376 KR2612.F C C42038 C42038 Vuji A1119961 uC23c06.r BB420958 BB420958 BB55089 BB420958 BB56089 BB56089 BF5501 RPCI11.16K9 BB56089 BB56089 BF5501 RPCI11.16K9 BB56089 BB56089 BF5501 RPCI11.16K9 BB56080 BB56089 BF5501 RPCI11.16K9 BB5810 RPCI23-A1-BB3-BB56089 BF5501 RPCI11.16K9 BB5810 BB58108 BF8914907 IL5-C1014 AA238189 RPCI-23-7 AV195887 AV195887 AV195887 AV195887 AV195887 AV195887 AV195887 AV195887 AV19451 AV191 C43142 C43141 Vuji C43142 C4318 Vuji C4318 C48718 Vuji C43783 C43783 Vuji C43783 C43783 Vuji R38942 Yd06f11.s1 R38942 Yd06f11.s1 R38942 Yd06f11.s1 R38942 AV193885 C4761 C4761 Vuji C48718 C4761 Vuji C48718 C4761 Vuji C48718 C4761 Vuji C48718 C4761 Vuji AV193885 AV193885 C47641 C47641 Vuji AV193301 AV193301 B41868-RICS4620A R	EST 28-AUG-1996 9.5 Mus musculus cDNA clone Craniata: Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus. Bowles, M., Dietrich, N., Dubuque, T., Le, M., Martin, J., Morris, M., 'an, F., Underwood, K., Moore, B., G., Soares, B., Wilson, R. and
Query Match Length DB ID Match Length DB ID 147 1 A038484 92.0 154 174 BG159502 92.0 1592 164 BE171588 92.0 215 216 188 R74725 92.0 216 188 R74725 92.0 216 188 R74725 92.0 221 4 A231776 92.0 221 133 BB420958 92.0 240 156 BB4200958 92.0 240 156 BB4200958 92.0 240 156 BB4200958 92.0 240 156 BB4200958 92.0 240 156 A1119961 92.0 324 159 BB420958 92.0 324 159 BB420958 92.0 324 159 BB420958 92.0 324 159 BB420958 92.0 326 156 C42110 92.0 360 156 C42110 92.0 372 17 A1206294 92.0 372 17 A1206294 92.0 372 17 A1206294 92.0 372 17 A1206294 92.0 373 187 R38943 92.0 375 26 AV193301 92.0 375 26 AV193301 92.0 377 26 AV193301 92.0 377 26 AV19888	MAN38484 147 bp mRNA EST 28-AUG-1996 mi83c09.rl Soares mouse p3NMF19.5 Mus musculus cDNA clone AA038484. AA038484.1 GI:1513891 EST. house mouse. house mouse. Was musculus Eutheria: Rodentia: Craniata: Vertebrata: Euteleostomi: Mammalia: Eutheria: Rodentia: Sciurognathi: Muridae: Musimusculus Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T Gelsel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and

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RESULT 1 AA038484/c LOCUS DEFINITION

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS

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